

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 19:45:33 ; Search time 8337 Seconds
(without alignments)
1147.582 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895
Sequence: 1 gtttagggcggtgtgtcc.....tggtgatcttcaaaaaaaaa 1895

Scoring table: OLIGO_NUC
Gapop_60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1886	99.5	1886	9	AB051833 Homo sapi
2	1780	94.5	1889	9	BC033010 Homo sapi
3	1742	91.9	1912	6	BD268022 Proteases
4	1484	78.8	1889	6	BD192303 Secreted
5	1284	67.8	1892	6	BD136402 95 human
6	719	37.9	2289	6	CQ722423 Sequence
7	528	27.9	964	6	BD139445 Extended
8	471	24.9	56580	2	AC135892 Homo sapi
9	471	24.9	245880	2	AC079387 Homo sapi
10	339	17.9	516	9	H006281 Homo sapi
11	281	14.8	308	6	BD060281 Secreted
12	280	14.8	507	6	BD179252 Cancer as
13	280	14.8	522	6	BD179034 Cancer as
14	149	7.9	391	11	G23540 human STS W
15	112	5.9	128	6	AX968632 Sequence
16	112	5.9	128	6	BD073650 5'EST of
17	71	3.7	316	6	AR415759 Sequence
18	71	3.7	316	6	AX972593 Sequence
19	71	3.7	316	6	BD111312 EST and e

20	60	3.2	60	6	CQ552626 Sequence
21	46	2.4	1813	4	PIGACRSN
22	46	2.4	1841	10	MUSP32A
23	46	2.4	166392	10	AC134529
24	34	1.8	261384	2	AC115415
25	32	1.7	1880	10	GPACRSN
26	27	1.4	29	6	BD192313 Secreted
27	26	1.4	1284	10	BC079212
28	24	1.3	66955	2	AC127516
29	24	1.3	67078	2	AC100227
30	24	1.3	156599	2	AC083840
31	24	1.3	190809	9	AC129908
32	24	1.3	198895	2	AP001337
33	24	1.3	204584	10	AC122243
34	24	1.3	204623	2	AP001338
35	24	1.3	215127	10	AC113542
36	24	1.3	215676	2	AC131299
37	24	1.3	221944	2	AC119914
38	23	1.2	2941	5	BC047248
39	23	1.2	2941	5	XL085969
40	23	1.2	2947	5	BC074454
41	23	1.2	198392	10	AL603745
42	23	1.2	225503	2	AC112301
43	23	1.2	231912	2	AC087566
44	23	1.2	232717	2	AC094171
45	22	1.2	234746	10	CNS080CAS
46	22	1.2	658	10	BC061122
47	22	1.2	1253	10	MUSP32B
48	22	1.2	1534	10	BC011079
49	22	1.2	1638	11	BV007555
50	22	1.2	28124	8	AP006410
51	22	1.2	67573	2	AC122760
52	22	1.2	100559	8	ATAC018363
53	22	1.2	112104	2	AC140155
54	22	1.2	124236	10	AL935312
55	22	1.2	173358	2	AC145050
56	22	1.2	175552	10	AC101691
57	22	1.2	181066	2	AC144606
58	22	1.2	183707	2	AY178785
59	22	1.2	184088	10	AC109305
60	22	1.2	184577	10	AC101728
61	22	1.2	193725	10	AC121575
62	22	1.2	198374	2	AC118519
63	22	1.2	200368	9	AC096541
64	22	1.2	215816	2	AC134937
65	22	1.2	222938	2	AC095075
66	22	1.2	226225	2	AC121002
67	22	1.2	236871	2	AC114108
68	22	1.2	251550	2	AC133772
69	22	1.2	259204	2	AC095370
70	22	1.2	299543	2	AC106692
71	21	1.1	450	6	AX778819
72	21	1.1	1053	4	AL831836
73	21	1.1	2411	6	CQ726297
74	21	1.1	2435	9	HSMB01140
75	21	1.1	2450	9	BC0001751
76	21	1.1	2525	5	BC067984
77	21	1.1	2684	9	BC019311
78	21	1.1	27645	10	AB075899
79	21	1.1	47300	9	HSMTM1
80	21	1.1	47405	2	AC136789
81	21	1.1	55516	2	AC101274
82	21	1.1	59767	6	CO870186
83	21	1.1	76982	9	AL731552
84	21	1.1	82082	8	AP006394
85	21	1.1	109092	10	AL928803
86	21	1.1	112354	2	AC101605
87	21	1.1	125922	9	AL731566
88	21	1.1	134482	2	AC0007335
89	21	1.1	145208	2	AC132921
90	21	1.1	153192	9	HSB234K24
91	21	1.1	158383	2	AC140161
92	21	1.1	158972	2	CR752649

C 93	21	1.1	161419	2	AC136927	AC136927 Homo sapi	C 166	20	1.1	7362	6	AR022379	AR022379 Sequence
C 94	21	1.1	166719	9	AC136957	AC136957 Homo sapi	C 167	20	1.1	7362	6	AR063882	AR063882 Sequence
C 95	21	1.1	172280	9	AL339879	AL339879 Human DNA	C 168	20	1.1	7362	6	AR067882	AR067882 Sequence
C 96	21	1.1	173595	2	AC020766	AC020766 Homo sapi	C 169	20	1.1	7362	6	AR105183	AR105183 Sequence
C 97	21	1.1	174452	2	AC142369	AC142369 Rattus no	C 170	20	1.1	7362	6	AR431823	AR431823 Sequence
C 98	21	1.1	175199	10	AL844480	AL844480 Homo sapi	C 171	20	1.1	7362	6	AR198608	AR198608 Sequence
C 99	21	1.1	175465	2	AL356783	AL356783 Mouse DNA	C 172	20	1.1	7364	6	AX333697	AX333697 Sequence
C 100	21	1.1	175750	10	AC134542	AC134542 Homo sapi	C 173	20	1.1	7364	6	AR198608	AR198608 Sequence
C 101	21	1.1	176250	2	AC148564	AC148564 Mus muscu	C 174	20	1.1	7364	6	AR198608	AR198608 Sequence
C 102	21	1.1	180424	2	AC102338	AC102338 Mus muscu	C 175	20	1.1	7364	6	AR198608	AR198608 Sequence
C 103	21	1.1	185895	2	AC150732	AC150732 Mus muscu	C 176	20	1.1	7364	6	AR198608	AR198608 Sequence
C 104	21	1.1	188394	2	AC121083	AC121083 Mus muscu	C 177	20	1.1	7364	6	AR198608	AR198608 Sequence
C 105	21	1.1	191886	9	AC084200	AC084200 Mus muscu	C 178	20	1.1	7364	6	AR198608	AR198608 Sequence
C 106	21	1.1	198434	9	AC102994	AC102994 Homo sapi	C 179	20	1.1	7364	6	AR198608	AR198608 Sequence
C 107	21	1.1	199204	2	AC131298	AC131298 Homo sapi	C 180	20	1.1	7364	6	AR198608	AR198608 Sequence
C 108	21	1.1	202334	2	AC131815	AC131815 Rattus no	C 181	20	1.1	7364	6	AR198608	AR198608 Sequence
C 109	21	1.1	202732	2	AC133745	AC133745 Rattus no	C 182	20	1.1	7364	6	AR198608	AR198608 Sequence
C 110	21	1.1	207521	2	AC136980	AC136980 Rattus no	C 183	20	1.1	7364	6	AR198608	AR198608 Sequence
C 111	21	1.1	209336	10	AC108840	AC108840 Mus muscu	C 184	20	1.1	7364	6	AR198608	AR198608 Sequence
C 112	21	1.1	211815	2	CR753872	CR753872 Dario fer	C 185	20	1.1	7364	6	AR198608	AR198608 Sequence
C 113	21	1.1	212290	5	BX005237	BX005237 Zebrafish	C 186	20	1.1	7364	6	AR198608	AR198608 Sequence
C 114	21	1.1	214202	10	AC123624	AC123624 Mus muscu	C 187	20	1.1	7364	6	AR198608	AR198608 Sequence
C 115	21	1.1	215435	2	AC126275	AC126275 Mus muscu	C 188	20	1.1	7364	6	AR198608	AR198608 Sequence
C 116	21	1.1	231411	2	AC059732	AC059732 Rattus no	C 189	20	1.1	7364	6	AR198608	AR198608 Sequence
C 117	21	1.1	238887	2	AC109745	AC109745 Rattus no	C 190	20	1.1	7364	6	AR198608	AR198608 Sequence
C 118	21	1.1	248880	2	AC109745	AC109745 Rattus no	C 191	20	1.1	7364	6	AR198608	AR198608 Sequence
C 119	21	1.1	248880	2	AC111302	AC111302 Rattus no	C 192	20	1.1	7364	6	AR198608	AR198608 Sequence
C 120	21	1.1	249444	2	AC112021	AC112021 Rattus no	C 193	20	1.1	7364	6	AR198608	AR198608 Sequence
C 121	21	1.1	259354	2	AC128889	AC128889 Rattus no	C 194	20	1.1	7364	6	AR198608	AR198608 Sequence
C 122	21	1.1	259354	2	AC126716	AC126716 Rattus no	C 195	20	1.1	7364	6	AR198608	AR198608 Sequence
C 123	21	1.1	269855	2	AC127669	AC127669 Rattus no	C 196	20	1.1	7364	6	AR198608	AR198608 Sequence
C 124	21	1.1	271603	2	AC106318	AC106318 Rattus no	C 197	20	1.1	7364	6	AR198608	AR198608 Sequence
C 125	21	1.1	291061	2	AC099169	AC099169 Rattus no	C 198	20	1.1	7364	6	AR198608	AR198608 Sequence
C 126	21	1.1	314421	2	AC104040	AC104040 Rattus no	C 199	20	1.1	7364	6	AR198608	AR198608 Sequence
C 127	21	1.1	317847	2	AC110430	AC110430 Rattus no	C 200	20	1.1	7364	6	AR198608	AR198608 Sequence
C 128	21	1.1	426	12	AY648613	AY648613 Mus muscu	C 201	20	1.1	7364	6	AR198608	AR198608 Sequence
C 129	20	1.1	466	6	CQ138089	CQ138089 Sequence	C 202	20	1.1	7364	6	AR198608	AR198608 Sequence
C 130	20	1.1	466	6	CQ221488	CQ221488 Sequence	C 203	20	1.1	7364	6	AR198608	AR198608 Sequence
C 131	20	1.1	466	6	CQ297309	CQ297309 Sequence	C 204	20	1.1	7364	6	AR198608	AR198608 Sequence
C 132	20	1.1	738	6	CQ821898	CQ821898 Sequence	C 205	20	1.1	7364	6	AR198608	AR198608 Sequence
C 133	20	1.1	792	6	AR390157	AR390157 Sequence	C 206	20	1.1	7364	6	AR198608	AR198608 Sequence
C 134	20	1.1	1038	5	CR352924	CR352924 Gallus ga	C 207	20	1.1	7364	6	AR198608	AR198608 Sequence
C 135	20	1.1	1102	8	AY059133	AY059133 Arabidops	C 208	20	1.1	7364	6	AR198608	AR198608 Sequence
C 136	20	1.1	1264	5	AF288369	AF288369 Gallus ga	C 209	20	1.1	7364	6	AR198608	AR198608 Sequence
C 137	20	1.1	1384	8	ATSP41	ATSP41 Arabidops	C 210	20	1.1	7364	6	AR198608	AR198608 Sequence
C 138	20	1.1	1400	8	AR370171	AR370171 Arabidops	C 211	20	1.1	7364	6	AR198608	AR198608 Sequence
C 139	20	1.1	1521	10	BC021362	BC021362 Mus muscu	C 212	20	1.1	7364	6	AR198608	AR198608 Sequence
C 140	20	1.1	1701	6	AR390279	AR390279 Sequence	C 213	20	1.1	7364	6	AR198608	AR198608 Sequence
C 141	20	1.1	1715	10	BC045146	BC045146 Mus muscu	C 214	20	1.1	7364	6	AR198608	AR198608 Sequence
C 142	20	1.1	1752	5	CR524204	CR524204 Gallus ga	C 215	20	1.1	7364	6	AR198608	AR198608 Sequence
C 143	20	1.1	1797	8	AK071584	AK071584 Oryza sat	C 216	20	1.1	7364	6	AR198608	AR198608 Sequence
C 144	20	1.1	2470	6	CO610649	CO610649 Sequence	C 217	20	1.1	7364	6	AR198608	AR198608 Sequence
C 145	20	1.1	3094	6	AY174486	AY174486 Sequence	C 218	20	1.1	7364	6	AR198608	AR198608 Sequence
C 146	20	1.1	3471	9	AK038657	AK038657 Homo sapi	C 219	20	1.1	7364	6	AR198608	AR198608 Sequence
C 147	20	1.1	3581	9	BC038669	BC038669 Homo sapi	C 220	20	1.1	7364	6	AR198608	AR198608 Sequence
C 148	20	1.1	4464	10	AY134612	AY134612 Mus muscu	C 221	20	1.1	7364	6	AR198608	AR198608 Sequence
C 149	20	1.1	4464	10	AY134612	AY134612 Mus muscu	C 222	20	1.1	7364	6	AR198608	AR198608 Sequence
C 150	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 223	20	1.1	7364	6	AR198608	AR198608 Sequence
C 151	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 224	20	1.1	7364	6	AR198608	AR198608 Sequence
C 152	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 225	20	1.1	7364	6	AR198608	AR198608 Sequence
C 153	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 226	20	1.1	7364	6	AR198608	AR198608 Sequence
C 154	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 227	20	1.1	7364	6	AR198608	AR198608 Sequence
C 155	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 228	20	1.1	7364	6	AR198608	AR198608 Sequence
C 156	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 229	20	1.1	7364	6	AR198608	AR198608 Sequence
C 157	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 230	20	1.1	7364	6	AR198608	AR198608 Sequence
C 158	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 231	20	1.1	7364	6	AR198608	AR198608 Sequence
C 159	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 232	20	1.1	7364	6	AR198608	AR198608 Sequence
C 160	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 233	20	1.1	7364	6	AR198608	AR198608 Sequence
C 161	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 234	20	1.1	7364	6	AR198608	AR198608 Sequence
C 162	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 235	20	1.1	7364	6	AR198608	AR198608 Sequence
C 163	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 236	20	1.1	7364	6	AR198608	AR198608 Sequence
C 164	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 237	20	1.1	7364	6	AR198608	AR198608 Sequence
C 165	20	1.1	5465	10	AY134612	AY134612 Mus muscu	C 238	20	1.1	7364	6	AR198608	AR198608 Sequence

GCCCTCAGAGGCCA-GCCTGACAGCGGC-AACAAATGGCAACCTCCCAAGAAGCT-CCCTTTTCAAGCCTT
 |||||
 GCCTCTC--AGGCACAGGAGCTTGGAAAGTCTGCGCGTTCTGTACACTGAAGTGGGGGTAGATGGGGAGGCTCAT
 |||||
 430 440 450 460 470 480 490
 TGCCTGACCTCCAGAGGCTCTCTTCATCTGGCAACACAGGTAAAGGCTCCCCAGAAATCAAGGCGGCTTTTAAAGGCGTGG
 |||||
 --CGTG-GTGGGTTGAAGCT-TT-AACCTG-AAAGCTCTTA---TCTCTCT
 |||||
 500 510 520
 ATTGTACGGTGGGCTCCACATGAGC
 |||||
 1350 1360
 X

> 0 <
0 | 0 IntelliGenetics
> 0 <

GENALIGN - Multiple Sequence Alignment Program Release 5.4

Wed 9 Mar 105 16:01:59- PST

Solution Parameters:

Nucleic Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off

AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

13. US-09-559-013E-23 (1-1895)
23. US-09-559-013E-33 (1-529)

Region Alignment: (listed in clustered order)

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US-09-559- 1 gtagagcggtgtgtgtcaccgagcgcgagctctccggccatgaggagccag
US-09-559- 1
US-09-559- 1 gtagagcggtgtgtgtcaccgagcgcgagctctccggccatgaggagccag
consensus gtagagcggtgtgtgtcaccgagcgcgagctctccggccatgaggagccag

US-09-559- 62 ccgctggtcttcctccctcactcctgaagtgctgctcctcctgacactgacgagc
US-09-559- 1
consensus ccgctggtcttcctccctcactcctgaagtgctgctcctcctgacactgacgagc

US-09-559- 123 ccaggaatcgactcagggcccccaactccagcgagcctctcctaccgaatacgaaagc
US-09-559- 1
consensus ccaggaatcgactcagggcccccaactccagcgagcctctcctaccgaatacgaaagc

US-09-559- 184 ttcttcgactgttgactccaactggaagcgagagactacgtcgtctccgtgcaacc
US-09-559- 1
consensus ttcttcgactgttgactccaactggaagcgagagactacgtcgtctccgtgcaacc

US-09-559- 245 acggctgcgggaatcccaactcgtccagctggaaccaatagaaacacaggttaagtgc
US-09-559- 1
consensus acggctgcgggaatcccaactcgtccagctggaaccaatagaaacacaggttaagtgc

US-09-559- 306 cgatgctgctgtcgtcctcaaccccttaagctcctggtttgagtccttctcaggttc
US-09-559- 1
consensus cgatgctgctgtcgtcctcaaccccttaagctcctggtttgagtccttctcaggttc

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US-09-559- 367 actcactaccgttgctcccaaccagctcactatgccaaagagtcctgtgttccacgacg
US-09-559- 9          CTCGA          gTAgagttcctcctatatttccatctt
consensus actcactaccgttgctcccaaccagctccta-TA-G-----A-----TTC-----

US-09-559- 428 tctctattcttcacctaaccatctcaaggagatagaagcttcagctgaagcttcaaccac
US-09-559- 46 catctattt
consensus --TCTATTctcttcacctaaccatctcaaggagatagaagcttcagctgaagcttcaaccac

US-09-559- 489 cagatgacctcccccatctcaaccacattcacagtgacagaagccagacctccagccc
US-09-559- 54          tcc
consensus cagatgacctcccccatctcaaccacattcacagtgacagaagccagacctccag-CC

US-09-559- 550 TGcCTGAgaggtccagcaacaacgctggaagAGCTCCTacaatcctctgtCccTgggAg
US-09-559- 57 TGcGCTGA          tcaatAGGCTCCT          ggaTgtTctcCattatcAt
consensus TGc-CTGAgaggtccagcaacaac--G-A-GAGCTCCTaca---T--T--C--T--A-

US-09-559- 611 gccAGAGcaagcgCcaagcacaagcAGAGCAAGaggtgagcaagagccgagc
US-09-559- 98 aggAGtAGactctactctcgtaccggGGAGCAA
consensus ---AG-AG-----C-----GAGCAAGaggtgagcaagagccgagc

US-09-559- 672 acaagaacacacagcaggaagaggggcagaaacagaaagcAAAGAGAGgaagag
US-09-559- 133          AAAGAGAA
consensus acaagaacacacagcaggaagaggggcagaaacagaaagcAAAGAGAGgaagag

US-09-559- 733 gagggaaagcAGAGAGgaaggggactaaggagggagcgggtgtgtcaggtgc
US-09-559- 141          gggctAGAAg
consensus gagggaaag--G--AGAGgaaggggactaaggagggagcgggtgtgtcaggtgc

US-09-559- 794 AGAGAGCTCAGAGccAGTTtcaCTTGAatctctatcttcaacccttcctcttgc
US-09-559- 151 AtAGAGatTCAGAGtgaaAaCTTggCTTGA
consensus A-A-AGA-TCAGAG---AA-TT---CTTGAatctctatcttcaacccttcctcttgc

US-09-559- 855 tccccgggtacgagagtagaGTTactcctatgatatgagaaatccagggatccat
US-09-559- 182          GTCT
consensus tccccgggtacgagagtagaGTTactcctatgatatgagaaatccagggatccat

US-09-559- 916 cgatcagccaggaatagatgaatgaatgaatgatgagaaatcctactggagaa
US-09-559- 186
consensus cgatcagccaggaatagatgaatgaatgaatgatgagaaatcctactggagaa

US-09-559- 977 accaaaacctggcagcttctGCAAGTgcccCAAGAGggccttgctgtgtgcta

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US-09-559- 186          GTCCTGCACTG  AGACACAG
consensus      accaaaacctggcagct--CTGCAAGCTGcc--ACACAGAGgacctgtgctgtgtgtcta

US-09-559- 1038  ttcgactcgtgGagaaATaCTgcacATaataccCCcaagCCcaagcCTcgaagtacatggag
US-09-559- 205      cctccGctcccttCCTtAgctCCctgtCCTctctccGcttCCctccctctccctt
consensus      ttcg-----G-----T-C-T-----C-----CC-----C-----C-----G--

US-09-559- 1099  gaagagatTccttggTttccGgaagtGggtctgtgacagcctTggGcggaacaatgCTa
US-09-559- 262  cctctcttgccttctctctGctGcttccGctccctctccctgtgtgttcttctgtcgcctCTg
consensus      -----T--T--T--G-----C-----T-----TG--C-----CT--

US-09-559- 1160  CCTGTGccctcTgtgacttctTGCTCTTgaagctggagagcATGcCATcagaagcagcCT
US-09-559- 323  CCTGTGc      TccactcctTgCTCTT      gcttGgc      tctggcgctgtctCCT
consensus      CCTGTGccctcT-----TGCTCCTTgaagctgg-----GNGcc-CT-----CCT

US-09-559- 1221  GcagcgGcaacaatgcgacacctcccaagaactcccttgtcagcccttgccttGCTCC
US-09-559- 370  G
consensus      GcagcgGcaacaatgcgacacctcccaagaactcccttgtcagcccttgccttGCTCC
                                     |||||
US-09-559- 1282  CAGagcctgtccAtcGgAaaccagGTAGggtcccccAGaAacagcCGcCTTcacGggtcg
US-09-559- 377  CAG      ggAcaagGAggagatcGTAGg      AgctcttCCaGgTgttGctgAc
consensus      CAGagcctgt--A---G-A-----GTAGggtcccccagA-----CC-C-TT---G---G-

US-09-559- 1343  aTTtgaacggTGGGCTccacatGgActTCTGctgtgccggtcttgCcaagaaaggCTGTGA
US-09-559- 423  ctctcagggcaGgGcT      ggaAggtCTGg      GgttcgtacCTGTGA
consensus      -T-T-----GGGCTccaca-G-A--TCTGctgtgccggtcttgC-----CTGTGA

US-09-559- 1404  AGatgtccgagctctcTGGGtgctccagactgagttccttagcttccagGATGGGaatctc
US-09-559- 466  AG      tggGgTg      aGAtGGGg
consensus      AGatgtccgagctcT--GGGTgtctccagactgagttccttagcttcca-GATGGGaatctc

US-09-559- 1465  cctacaagatltgtgacacagactatctccagtaaccaactactgttcccttcaaaagcc
US-09-559- 483
consensus      cctacaagatltgtgacacagactatctccagtaaccaactactgttcccttcaaaagcc

US-09-559- 1526  agcagtgctgtgAtbagaacCGcAATCGgaagGTGtcccgcatgagatgtctgcagaatGA
US-09-559- 483      gagGcATNG      tGGTg      gGTGA
consensus      agcagtgctgtgAtgagaa---G--ATCGga-GGTGtcccgcatgagatgtctgcag--TGA

US-09-559- 1587  GACTTAcagtgcgctgagccctcgcaaaagtgaagacgttggtctcgatggaGCCagag
US-09-559- 503  GACTT
consensus      GACTTAcagtgcgctgagccctcgcaaaagtgaagacgttggtctcgatggaGCCagag

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US-09-559- 1648  ttcagacacttgactctagaccaggtcggatgAGCTGcggtctcatctctgtcccaaccaccag
US-09-559- 508      |||||
consensus      ttcagacacttgactctagaccaggtcggat-AGCTGcggtctcatctctgtcccaaccaccag
                                     |||||
US-09-559- 1709  cccaacctggcccaagctcCTATtgttcttgagaccccatgtgcttcaaggctgccccctctg
US-09-559- 514      aagctCTAT
consensus      cccaacctggccca-----TCTATtgttcttgagaccccatgtgcttcaaggctgccccctctg

US-09-559- 1770  ggtctgttactcgccctactacatcttcccttgggttgagacaagtcctccagaagggc
US-09-559- 524
consensus      ggtctgttactcgccctactacatcttcccttgggttgagacaagtcctccagaagggc

US-09-559- 1831  caGgTgGgagctgcgcCTCCTTaaagatgacttcaabaaatgtgatcttcaaaaa
US-09-559- 524      |||||
consensus      caGgTgGgagctgcgcCTCCTTaaagatgacttcaabaaatgtgatcttcaaaaa
                                     CTGCTT

US-09-559- 1892  aaaa
US-09-559- 530
consensus      aaaa

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Alignment score = -6577.00

Scoring matrix:

13		13
	-6643	
23		23

239	20	1.1	174952	9	AC002460	AC002460 Human BAC	C 312	20	1.1	238861	2	AC148331	AC148331 Mus muscu
240	20	1.1	175251	2	AC101838	AC101838 Mus muscu	313	20	1.1	240584	2	AC116063	AC116063 Rattus no
241	20	1.1	175302	9	AL355677	Human DNA	C 314	20	1.1	241086	2	AC106653	AC106653 Rattus no
242	20	1.1	175360	2	AC018948	AC018948 Homo sapi	C 315	20	1.1	242195	2	AC126644	AC126644 Rattus no
243	20	1.1	175491	2	AC129683	AC129683 Rattus no	C 316	20	1.1	242510	2	AC128507	AC128507 Rattus no
244	20	1.1	175639	10	AC132557	AC132557 Mus muscu	C 317	20	1.1	243306	2	AC130628	AC130628 Rattus no
245	20	1.1	176372	2	AC026030	AC026030 Homo sapi	C 318	20	1.1	244451	2	AC125765	AC125765 Rattus no
246	20	1.1	176889	10	AC124830	AC124830 Mus muscu	C 319	20	1.1	245496	10	AC109204	AC109204 Mus muscu
247	20	1.1	176915	9	AC008050	AC008050 Homo sapi	C 320	20	1.1	245971	2	AC133446	AC133446 Rattus no
248	20	1.1	177115	9	AC091805	AC091805 Homo sapi	C 321	20	1.1	249068	2	AC095295	AC095295 Rattus no
249	20	1.1	177483	9	AC068233	AC068233 Homo sapi	C 322	20	1.1	250688	2	AC094683	AC094683 Rattus no
250	20	1.1	177952	10	AC113033	AC113033 Mus muscu	C 323	20	1.1	251866	2	AC120750	AC120750 Rattus no
251	20	1.1	178380	2	AC129819	AC129819 Rattus no	C 324	20	1.1	251194	2	AC103307	AC103307 Rattus no
252	20	1.1	178523	8	AC135561	AC135561 Oryza sat	C 325	20	1.1	253149	2	AC107527	AC107527 Rattus no
253	20	1.1	182071	9	AC103740	AC103740 Homo sapi	C 326	20	1.1	254452	2	AC118338	AC118338 Rattus no
254	20	1.1	183577	2	AC011164	AC011164 Homo sapi	C 327	20	1.1	254646	2	AC109890	AC109890 Rattus no
255	20	1.1	184365	2	AC079659	AC079659 Mus muscu	C 328	20	1.1	255239	2	AC109676	AC109676 Rattus no
256	20	1.1	184738	9	AL162574	AL162574 Human DNA	C 329	20	1.1	256229	2	AC073676	AC073676 Mus muscu
257	20	1.1	185855	5	CR759734	CR759734 Zebrafish	C 330	20	1.1	269739	10	AC139108	AC139108 Mus muscu
258	20	1.1	186205	10	AC140336	AC140336 Mus muscu	C 331	20	1.1	271600	2	AC107601	AC107601 Rattus no
259	20	1.1	186330	9	AC007376	AC007376 Homo sapi	C 332	20	1.1	271932	2	AC109948	AC109948 Rattus no
260	20	1.1	187540	9	AC126669	AC126669 Mus muscu	C 333	20	1.1	289782	2	AC151297	AC151297 Mus muscu
261	20	1.1	189091	2	AC118207	AC118207 Mus muscu	C 334	20	1.1	290248	2	AC094662	AC094662 Rattus no
262	20	1.1	189924	2	AC119533	AC119533 Mus muscu	C 335	20	1.1	293412	2	AC133037	AC133037 Rattus no
263	20	1.1	190853	5	BX005041	BX005041 Zebrafish	C 336	20	1.1	313096	2	AC113536	AC113536 Mus muscu
264	20	1.1	192169	2	AC020849	AC020849 Mus muscu	C 337	20	1.1	337636	2	AE003584	AE003584 Drosophila
265	20	1.1	192619	2	AC122789	AC122789 Mus muscu	C 338	20	1.1	349980	6	AX781290	AX781290 Sequence
266	20	1.1	193212	9	AP004370	AP004370 Homo sapi	C 339	19	1.0	352	3	AY619275	AY619275 Daphnia p
267	20	1.1	193380	2	AC013370	AC013370 Homo sapi	C 340	19	1.0	367	6	AX916154	AX916154 Sequence
268	20	1.1	193939	2	AC113413	AC113413 Homo sapi	C 341	19	1.0	367	6	BD051687	BD051687 Sequence
269	20	1.1	194792	2	AC115931	AC115931 Mus muscu	C 342	19	1.0	378	6	CQ448501	CQ448501 Sequence
270	20	1.1	194937	9	BS000153	BS000153 Pan trogl	C 343	19	1.0	383	8	AF543707	AF543707 Botryosph
271	20	1.1	195742	2	AC151362	AC151362 Ictalurus	C 344	19	1.0	472	6	CO698066	CO698066 Sequence
272	20	1.1	196272	2	AC026675	AC026675 Homo sapi	C 345	19	1.0	530	8	AF464753	AF464753 Temarix p
273	20	1.1	196773	10	AC023613	AC023613 Mus muscu	C 346	19	1.0	578	8	AB065389	AB065389 F11obasid
274	20	1.1	197131	2	AC121829	AC121829 Mus muscu	C 347	19	1.0	580	6	AR412990	AR412990 Sequence
275	20	1.1	199519	10	AC121872	AC121872 Mus muscu	C 348	19	1.0	580	6	AX969824	AX969824 Sequence
276	20	1.1	200222	2	AC023555	AC023555 Homo sapi	C 349	19	1.0	580	6	BD108543	BD108543 EST and e
277	20	1.1	200265	2	AC099579	AC099579 Mus muscu	C 350	19	1.0	603	6	BD210354	BD210354 Human gen
278	20	1.1	200465	2	AC148786	AC148786 Oryzomys	C 351	19	1.0	634	11	G91812	G91812 S208P678RRE
279	20	1.1	202114	2	BX957272	BX957272 Danio rer	C 352	19	1.0	645	10	AY055379	AY055379 Rattus no
280	20	1.1	203159	10	AC137525	AC137525 Mus muscu	C 353	19	1.0	760	3	PMH1SH2B	PMH1SH2B X01344 Peamemchinu
281	20	1.1	203974	2	BX914220	BX914220 Danio rer	C 354	19	1.0	845	3	SUPH1SB2	SUPH1SB2 P.miliaris
282	20	1.1	204428	2	AC138019	AC138019 Papio anu	C 355	19	1.0	930	5	AF294666	AF294666 Heliomast
283	20	1.1	205580	2	AC101839	AC101839 Mus muscu	C 356	19	1.0	930	5	AF294667	AF294667 Hylochoari
284	20	1.1	207080	2	AC146149	AC146149 Pan trogl	C 357	19	1.0	930	5	AY065759	AY065759 Galliarria
285	20	1.1	209454	2	CR626940	CR626940 Danio rer	C 358	19	1.0	930	5	AY065750	AY065750 Hylopezus
286	20	1.1	211414	2	AC150057	AC150057 Gallus ga	C 359	19	1.0	930	5	AY339102	AY339102 Arenaria
287	20	1.1	211555	2	AC132172	AC132172 Rattus no	C 360	19	1.0	930	5	AY339114	AY339114 Phalaropa
288	20	1.1	211595	2	AC019334	AC019334 Homo sapi	C 361	19	1.0	930	5	AY339124	AY339124 Thinnocoru
289	20	1.1	211786	2	AC135516	AC135516 Rattus no	C 362	19	1.0	930	5	AY339125	AY339125 Tringa to
290	20	1.1	213085	2	AC095379	AC095379 Rattus no	C 363	19	1.0	945	6	CQ737591	CQ737591 Sequence
291	20	1.1	213683	10	AC109280	AC109280 Mus muscu	C 364	19	1.0	963	6	AX576131	AX576131 Sequence
292	20	1.1	213779	2	AC113958	AC113958 Mus muscu	C 365	19	1.0	1107	5	GGLAMP39	GGLAMP39 Z94718 G.gallus nr
293	20	1.1	213817	2	AC099865	AC099865 Mus muscu	C 366	19	1.0	1247	5	CR523041	CR523041 Gallus ga
294	20	1.1	215101	2	AC148847	AC148847 Oryzomys	C 367	19	1.0	1287	6	AR429815	AR429815 Sequence
295	20	1.1	215175	2	AC108664	AC108664 Rattus no	C 368	19	1.0	1289	8	AK071491	AK071491 Oryza sat
296	20	1.1	215849	2	AL590654	AL590654 Mus muscu	C 369	19	1.0	1289	8	AF458274	AF458274 Tritlicum
297	20	1.1	218644	9	AC147079	AC147079 Pan trogl	C 370	19	1.0	1364	8	SPH2B01	SPH2B01 X00146 Sea urchin
298	20	1.1	219486	2	AC116283	AC116283 Rattus no	C 371	19	1.0	1521	6	AR429826	AR429826 Sequence
299	20	1.1	221608	2	AC135934	AC135934 Rattus no	C 372	19	1.0	1632	9	AK024986	AK024986 Homo sapi
300	20	1.1	223952	10	AC107742	AC107742 Mus muscu	C 373	19	1.0	1713	6	AR375702	AR375702 Sequence
301	20	1.1	225310	2	AC150170	AC150170 Gallus ga	C 374	19	1.0	1729	8	AB088027	AB088027 Camellia
302	20	1.1	233772	2	AC115403	AC115403 Rattus no	C 375	19	1.0	1730	6	B39318	B39318 beta-Primev
303	20	1.1	234362	2	AC114567	AC114567 Mus muscu	C 376	19	1.0	1731	6	BD180525	BD180525 Highly th
304	20	1.1	234717	2	AC095194	AC095194 Rattus no	C 377	19	1.0	1914	5	AF294683	AF294683 Trachypno
305	20	1.1	235326	2	AC105692	AC105692 Rattus no	C 378	19	1.0	1914	5	AF294684	AF294684 Staccollae
306	20	1.1	235794	2	AC151298	AC151298 Mus muscu	C 379	19	1.0	1914	5	AF295195	AF295195 Picumnus
307	20	1.1	235868	10	AL645947	AL645947 Mouse DNA	C 380	19	1.0	1914	5	AY165794	AY165794 Indicator
308	20	1.1	236010	2	AC151268	AC151268 Mus muscu	C 381	19	1.0	1934	5	AK026807	AK026807 Homo sapi
309	20	1.1	236951	2	AC098662	AC098662 Rattus no	C 382	19	1.0	1949	10	BC029741	BC029741 Mus muscu
310	20	1.1	237720	2	AC132559	AC132559 Rattus no	C 383	19	1.0	1951	5	BC049336	BC049336 Danio rer
311	20	1.1	238390	2	AC117035	AC117035 Rattus no	C 384	19	1.0	2000	6	AX461161	AX461161 Sequence

C 385	19	1.0	2000	6	AX508752	AX508752 Sequence	458	19	1.0	9743	14	AF435866	AF435866 Rubella v
C 386	19	1.0	2011	10	AB039933	AB039933 Mus muscu	459	19	1.0	9755	14	RUBCG	M15240 Rubella v
C 387	19	1.0	2017	14	AF231105	AF231105 Bovine he	460	19	1.0	9759	6	163470	163470 Sequence 1
C 388	19	1.0	2033	3	SPHIS1	VO1356 Sea urchin	461	19	1.0	9762	6	AX009468	AX009468 Sequence
C 389	19	1.0	2033	3	SPHIS1	VO1356 Sea urchin	461	19	1.0	9762	14	AB047329	AB047329 Rubella v
C 390	19	1.0	2190	3	AY061073	AY061073 Drosophila	462	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 391	19	1.0	2228	6	AC000743	AC000743 Homo sapi	463	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 392	19	1.0	2236	6	AC000743	AC000743 Homo sapi	463	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 393	19	1.0	2305	5	BC084637	BC084637 Xenopus la	464	19	1.0	9762	14	AB047330	AB047330 Rubella v
C 394	19	1.0	2325	9	AB052096	AB052096 Homo sapi	465	19	1.0	17700	9	HSXBXVII	HSXBXVII
C 395	19	1.0	2352	3	AY118334	AY118334 Drosophila	466	19	1.0	13905	2	AL450407	AL450407 Homo sapi
C 396	19	1.0	2451	14	RUBIE2	RUBIE2	467	19	1.0	18106	9	AL450407	AL450407 Homo sapi
C 397	19	1.0	2464	10	MCANP3	MCANP3	468	19	1.0	27300	2	AC092450	AC092450
C 398	19	1.0	2466	10	MCANP3	MCANP3	469	19	1.0	32173	5	EX005325	EX005325
C 399	19	1.0	2570	6	BD276297	BD276297 Sequence	470	19	1.0	34796	5	EX005325	EX005325
C 400	19	1.0	2597	6	AX047352	AX047352 Sequence	471	19	1.0	35848	2	CEM01553	CEM01553
C 401	19	1.0	2632	3	BT004849	BT004849 Drosophila	472	19	1.0	35922	9	AC145124	AC145124
C 402	19	1.0	2653	3	BT004849	BT004849 Drosophila	473	19	1.0	36241	1	MT015186	MT015186
C 403	19	1.0	2655	10	MMU14103	MMU14103	474	19	1.0	36241	6	AR45366	AR45366
C 404	19	1.0	2665	6	BD157994	BD157994 Primer fo	475	19	1.0	36926	3	AR067616	AR067616
C 405	19	1.0	2665	6	AX879732	AX879732 Sequence	476	19	1.0	38066	3	U97549	U97549
C 406	19	1.0	2665	6	AX879732	AX879732 Sequence	477	19	1.0	40397	2	AC145174	AC145174
C 407	19	1.0	2671	6	AR075344	AR075344 Sequence	478	19	1.0	40726	2	AC145174	AC145174
C 408	19	1.0	2671	6	AR075344	AR075344 Sequence	479	19	1.0	40726	2	AC145174	AC145174
C 409	19	1.0	2671	6	AR075344	AR075344 Sequence	480	19	1.0	40726	2	AC145174	AC145174
C 410	19	1.0	2671	6	AR075344	AR075344 Sequence	481	19	1.0	40726	2	AC145174	AC145174
C 411	19	1.0	2671	6	AR075344	AR075344 Sequence	482	19	1.0	40726	2	AC145174	AC145174
C 412	19	1.0	2671	6	AR075344	AR075344 Sequence	483	19	1.0	40726	2	AC145174	AC145174
C 413	19	1.0	2671	6	AR075344	AR075344 Sequence	484	19	1.0	40726	2	AC145174	AC145174
C 414	19	1.0	2671	6	AR075344	AR075344 Sequence	485	19	1.0	40726	2	AC145174	AC145174
C 415	19	1.0	2671	6	AR075344	AR075344 Sequence	486	19	1.0	40726	2	AC145174	AC145174
C 416	19	1.0	2671	6	AR075344	AR075344 Sequence	487	19	1.0	40726	2	AC145174	AC145174
C 417	19	1.0	2671	6	AR075344	AR075344 Sequence	488	19	1.0	40726	2	AC145174	AC145174
C 418	19	1.0	2671	6	AR075344	AR075344 Sequence	489	19	1.0	40726	2	AC145174	AC145174
C 419	19	1.0	2671	6	AR075344	AR075344 Sequence	490	19	1.0	40726	2	AC145174	AC145174
C 420	19	1.0	2671	6	AR075344	AR075344 Sequence	491	19	1.0	40726	2	AC145174	AC145174
C 421	19	1.0	2671	6	AR075344	AR075344 Sequence	492	19	1.0	40726	2	AC145174	AC145174
C 422	19	1.0	2671	6	AR075344	AR075344 Sequence	493	19	1.0	40726	2	AC145174	AC145174
C 423	19	1.0	2671	6	AR075344	AR075344 Sequence	494	19	1.0	40726	2	AC145174	AC145174
C 424	19	1.0	2671	6	AR075344	AR075344 Sequence	495	19	1.0	40726	2	AC145174	AC145174
C 425	19	1.0	2671	6	AR075344	AR075344 Sequence	496	19	1.0	40726	2	AC145174	AC145174
C 426	19	1.0	2671	6	AR075344	AR075344 Sequence	497	19	1.0	40726	2	AC145174	AC145174
C 427	19	1.0	2671	6	AR075344	AR075344 Sequence	498	19	1.0	40726	2	AC145174	AC145174
C 428	19	1.0	2671	6	AR075344	AR075344 Sequence	499	19	1.0	40726	2	AC145174	AC145174
C 429	19	1.0	2671	6	AR075344	AR075344 Sequence	500	19	1.0	40726	2	AC145174	AC145174
C 430	19	1.0	2671	6	AR075344	AR075344 Sequence	501	19	1.0	40726	2	AC145174	AC145174
C 431	19	1.0	2671	6	AR075344	AR075344 Sequence	502	19	1.0	40726	2	AC145174	AC145174
C 432	19	1.0	2671	6	AR075344	AR075344 Sequence	503	19	1.0	40726	2	AC145174	AC145174
C 433	19	1.0	2671	6	AR075344	AR075344 Sequence	504	19	1.0	40726	2	AC145174	AC145174
C 434	19	1.0	2671	6	AR075344	AR075344 Sequence	505	19	1.0	40726	2	AC145174	AC145174
C 435	19	1.0	2671	6	AR075344	AR075344 Sequence	506	19	1.0	40726	2	AC145174	AC145174
C 436	19	1.0	2671	6	AR075344	AR075344 Sequence	507	19	1.0	40726	2	AC145174	AC145174
C 437	19	1.0	2671	6	AR075344	AR075344 Sequence	508	19	1.0	40726	2	AC145174	AC145174
C 438	19	1.0	2671	6	AR075344	AR075344 Sequence	509	19	1.0	40726	2	AC145174	AC145174
C 439	19	1.0	2671	6	AR075344	AR075344 Sequence	510	19	1.0	40726	2	AC145174	AC145174
C 440	19	1.0	2671	6	AR075344	AR075344 Sequence	511	19	1.0	40726	2	AC145174	AC145174
C 441	19	1.0	2671	6	AR075344	AR075344 Sequence	512	19	1.0	40726	2	AC145174	AC145174
C 442	19	1.0	2671	6	AR075344	AR075344 Sequence	513	19	1.0	40726	2	AC145174	AC145174
C 443	19	1.0	2671	6	AR075344	AR075344 Sequence	514	19	1.0	40726	2	AC145174	AC145174
C 444	19	1.0	2671	6	AR075344	AR075344 Sequence	515	19	1.0	40726	2	AC145174	AC145174
C 445	19	1.0	2671	6	AR075344	AR075344 Sequence	516	19	1.0	40726	2	AC145174	AC145174
C 446	19	1.0	2671	6	AR075344	AR075344 Sequence	517	19	1.0	40726	2	AC145174	AC145174
C 447	19	1.0	2671	6	AR075344	AR075344 Sequence	518	19	1.0	40726	2	AC145174	AC145174
C 448	19	1.0	2671	6	AR075344	AR075344 Sequence	519	19	1.0	40726	2	AC145174	AC145174
C 449	19	1.0	2671	6	AR075344	AR075344 Sequence	520	19	1.0	40726	2	AC145174	AC145174
C 450	19	1.0	2671	6	AR075344	AR075344 Sequence	521	19	1.0	40726	2	AC145174	AC145174
C 451	19	1.0	2671	6	AR075344	AR075344 Sequence	522	19	1.0	40726	2	AC145174	AC145174
C 452	19	1.0	2671	6	AR075344	AR075344 Sequence	523	19	1.0	40726	2	AC145174	AC145174
C 453	19	1.0	2671	6	AR075344	AR075344 Sequence	524	19	1.0	40726	2	AC145174	AC145174
C 454	19	1.0	2671	6	AR075344	AR075344 Sequence	525	19	1.0	40726	2	AC145174	AC145174
C 455	19	1.0	2671	6	AR075344	AR075344 Sequence	526	19	1.0	40726	2	AC145174	AC145174
C 456	19	1.0	2671	6	AR075344	AR075344 Sequence	527	19	1.0	40726	2	AC145174	AC145174
C 457	19	1.0	2671	6	AR075344	AR075344 Sequence	528	19	1.0	40726	2	AC145174	AC145174
C 458	19	1.0	2671	6	AR075344	AR075344 Sequence	529	19	1.0	40726	2	AC145174	AC145174
C 459	19	1.0	2671	6	AR075344	AR075344 Sequence	530	19	1.0	40726	2	AC145174	AC145174

531	19	1.0	92697	9	AL135784	604	19	1.0	129459	10	AF372979	Mus muscu
532	19	1.0	93717	9	AL357673	C 605	19	1.0	129811	9	HSB3477	AL049547 Human DNA
533	19	1.0	94027	9	AC073221	C 606	19	1.0	130515	10	AC117195	AL049547 Human DNA
534	19	1.0	94595	2	AL732591	C 607	19	1.0	130716	10	AC140109	AC140109 Mus muscu
535	19	1.0	94766	2	AC144930	C 608	19	1.0	130946	10	AC129310	AC129310 Mus muscu
536	19	1.0	95850	2	AC020063	C 609	19	1.0	131112	9	AL157712	AL157712 Human DNA
537	19	1.0	96245	2	AC087459	C 610	19	1.0	131570	9	AP002495	AP002495 Homo sapi
538	19	1.0	96335	9	BS679671	C 611	19	1.0	132978	2	AC097011	AC097011 Sus scrofa
539	19	1.0	97847	9	HS874C20	C 612	19	1.0	133337	2	AC016231	AC016231 Homo sapi
540	19	1.0	98593	9	AL356472	C 613	19	1.0	133267	2	AL157389	AL157389 Human DNA
541	19	1.0	99672	2	AC110531	C 614	19	1.0	134270	2	AC147762	AC147762 Dasyatis n
542	19	1.0	99908	9	AC006464	C 615	19	1.0	134697	9	AC114738	AC114738 Homo sapi
543	19	1.0	100000	9	AP000079	C 616	19	1.0	134904	9	AC004879	AC004879 Homo sapi
544	19	1.0	100267	2	HSBHC36A	C 617	19	1.0	135214	9	AC004848	AC004848 Homo sapi
545	19	1.0	100538	2	AC152813	C 618	19	1.0	135321	2	AC142021	AC142021 Rattus no
546	19	1.0	103488	10	AL772395	C 619	19	1.0	136002	9	AC120094	AC120094 Homo sapi
547	19	1.0	104907	9	HSB3741H3	C 620	19	1.0	136083	4	AC091656	AC091656 Felis cat
548	19	1.0	105239	9	AL339059	C 621	19	1.0	136581	9	AC008459	AC008459 Homo sapi
549	19	1.0	106004	1	AP006585	C 622	19	1.0	137013	2	AC151827	AC151827 Mus muscu
550	19	1.0	106806	2	AF165177	C 623	19	1.0	137263	2	AC068740	AC068740 Homo sapi
551	19	1.0	107132	4	BS255941	C 624	19	1.0	137263	2	AC068740	AC068740 Homo sapi
552	19	1.0	107413	5	AL773560	C 625	19	1.0	138278	9	AC137695	AC137695 Homo sapi
553	19	1.0	107532	9	AC010425	C 626	19	1.0	138313	9	AC092111	AC092111 Homo sapi
554	19	1.0	108873	14	AF318573	C 627	19	1.0	138938	2	AL928569	AL928569 Homo sapi
555	19	1.0	109099	2	AC143174	C 628	19	1.0	138932	9	AL662828	AL662828 Human DNA
556	19	1.0	109646	9	HSBHC822	C 629	19	1.0	139126	10	AC126608	AC126608 Mus muscu
557	19	1.0	110000	2	AC092450	C 630	19	1.0	140148	9	AL354916	AL354916 Human DNA
558	19	1.0	110000	2	AC092450	C 631	19	1.0	140292	9	CNS01D08	AL133223 Human chr
559	19	1.0	110000	2	AC097542	C 632	19	1.0	141456	9	AL355300	AL355300 Human DNA
560	19	1.0	110000	2	AC097542	C 633	19	1.0	141591	9	AC079467	AC079467 Homo sapi
561	19	1.0	110000	2	AC107427	C 634	19	1.0	141674	2	AC080046	AC080046 Homo sapi
562	19	1.0	110000	2	AC115281	C 635	19	1.0	142064	2	AC091193	AC091193 Homo sapi
563	19	1.0	110000	2	AC123006	C 636	19	1.0	142275	2	CR788316	CR788316 Danio rer
564	19	1.0	110000	2	AC123189	C 637	19	1.0	142467	2	AC022945	AC022945 Homo sapi
565	19	1.0	110000	2	AC125631	C 638	19	1.0	142560	2	CR753845	CR753845 Homo sapi
566	19	1.0	110000	2	AC130665	C 639	19	1.0	142711	8	AC087181	AC087181 Oryza sat
567	19	1.0	110000	8	CR382139	C 640	19	1.0	142728	5	BX005383	BX005383 Zebrafish
568	19	1.0	110000	9	AF491780	C 641	19	1.0	143958	2	AC141527	AC141527 Rattus no
569	19	1.0	110000	9	HS454950	C 642	19	1.0	144933	5	AL953847	AL953847 Zebrafish
570	19	1.0	110052	10	AL929268	C 643	19	1.0	145632	9	AL355303	AL355303 Human DNA
571	19	1.0	110116	9	AP001931	C 644	19	1.0	146000	9	AP005433	AP005433 Homo sapi
572	19	1.0	110283	9	AF298854	C 645	19	1.0	146022	9	AC026881	AC026881 Homo sapi
573	19	1.0	112140	10	BS321901	C 646	19	1.0	146310	9	AC090459	AC090459 Homo sapi
574	19	1.0	112168	9	BS572623	C 647	19	1.0	146332	2	AL603762	AL603762 Homo sapi
575	19	1.0	112339	9	HS110P11	C 648	19	1.0	147480	9	AC091639	AC091639 Homo sapi
576	19	1.0	112685	2	AC016592	C 649	19	1.0	147727	10	AL929001	AL929001 Mouse DNA
577	19	1.0	114518	2	CR753825	C 650	19	1.0	148846	10	AL591204	AL591204 Mouse DNA
578	19	1.0	115968	9	AL365277	C 651	19	1.0	149163	2	AC073835	AC073835 Homo sapi
579	19	1.0	116102	2	AC131236	C 652	19	1.0	149461	9	AC139453	AC139453 Homo sapi
580	19	1.0	116580	10	AC112162	C 653	19	1.0	149487	10	AC124110	AC124110 Mus muscu
581	19	1.0	117500	9	AC087203	C 654	19	1.0	149706	2	AC138050	AC138050 Mus muscu
582	19	1.0	117721	9	HS113J7	C 655	19	1.0	149965	9	AC007718	AC007718 Homo sapi
583	19	1.0	119082	2	AC008057	C 656	19	1.0	151271	5	BS511003	BS511003 Zebrafish
584	19	1.0	120301	9	AC135166	C 657	19	1.0	151492	9	CR376864	CR376864 Pan trogl
585	19	1.0	120464	5	AC091751	C 658	19	1.0	151805	2	AC013741	AC013741 Homo sapi
586	19	1.0	120637	10	CNS07P1	C 659	19	1.0	152515	10	AL928608	AL928608 Mouse DNA
587	19	1.0	120864	2	AC079884	C 660	19	1.0	152539	9	AC092745	AC092745 Homo sapi
588	19	1.0	121543	2	AL772350	C 661	19	1.0	152843	9	AC025828	AC025828 Homo sapi
589	19	1.0	122438	2	AC141125	C 662	19	1.0	153394	2	AP000727	AP000727 Homo sapi
590	19	1.0	122493	2	AC008583	C 663	19	1.0	153819	10	AC121955	AC121955 Mus muscu
591	19	1.0	124166	2	AC108920	C 664	19	1.0	154052	2	AC027099	AC027099 Mus muscu
592	19	1.0	124209	2	AC139876	C 665	19	1.0	154288	2	AC068778	AC068778 Homo sapi
593	19	1.0	124409	9	AC059360	C 666	19	1.0	154577	2	AC135458	AC135458 Homo sapi
594	19	1.0	124713	9	AC008620	C 667	19	1.0	154665	2	AC016334	AC016334 Homo sapi
595	19	1.0	125209	10	AC079871	C 668	19	1.0	154846	2	AC079009	AC079009 Homo sapi
596	19	1.0	125891	9	AF165423	C 669	19	1.0	155586	2	AP006245	AP006245 Homo sapi
597	19	1.0	126837	9	AL451106	C 670	19	1.0	155637	10	AC111012	AC111012 Mus muscu
598	19	1.0	127270	9	AC004740	C 671	19	1.0	155640	2	AC024454	AC024454 Homo sapi
599	19	1.0	127391	10	AL935327	C 672	19	1.0	155662	2	AC024454	AC024454 Homo sapi
600	19	1.0	128632	10	CNS07YOU	C 673	19	1.0	155869	2	AC023420	AC023420 Homo sapi
601	19	1.0	128822	2	AP001260	C 674	19	1.0	155904	2	AC015953	AC015953 Homo sapi
602	19	1.0	128910	10	AC125308	C 675	19	1.0	156033	9	AC137066	AC137066 Pan trogl
603	19	1.0	129302	2	AC083918	C 676	19	1.0	156054	9	HSB316705	AL121938 Human DNA

677	1.0	156210	2	AC016303	AC016303 Homo sapi	c 750	1.0	166365	10	AC129200	AC129200 Mus muscu
c 678	1.0	156425	5	BX276090	BX276090 Zebrafish	c 751	1.0	166486	5	CNS05TEN	AL153872 Human chr
c 679	1.0	156754	2	AC021364	AC021364 Homo sapi	c 752	1.0	166518	5	CR555301	CR555301 Zebrafish
c 680	1.0	156756	2	AC011134	AC011134 Homo sapi	c 753	1.0	166575	9	AC091989	AC091989 Homo sapi
c 681	1.0	157080	2	AC083981	AC083981 Homo sapi	c 754	1.0	166679	2	AC121551	AC121551 Mus muscu
c 682	1.0	157347	2	AC115008	AC115008 Mus muscu	c 755	1.0	166702	9	AC079018	AC079018 Homo sapi
c 683	1.0	157390	2	AC025366	AC025366 Homo sapi	c 756	1.0	166907	5	AP205406	AP205406 Homo sapi
c 684	1.0	157665	10	AC069018	AC069018 Homo sapi	c 757	1.0	166937	5	AP001024	AP001024 Zebrafish
c 685	1.0	158004	2	AL583833	AL583833 Mus muscu	c 758	1.0	166949	5	AC007630	AC007630 Homo sapi
c 686	1.0	158209	2	AC105214	AC105214 Homo sapi	c 759	1.0	166952	5	AC007630	AC007630 Homo sapi
c 687	1.0	158458	2	AC111155	AC111155 Homo sapi	c 760	1.0	166961	2	AC110425	AC110425 Homo sapi
c 688	1.0	158711	2	AC113510	AC113510 Strongylo	c 761	1.0	166961	2	AC110425	AC110425 Homo sapi
c 689	1.0	158829	2	AC130068	AC130068 Rattus no	c 762	1.0	166961	2	AC110425	AC110425 Homo sapi
c 690	1.0	158859	2	AC098657	AC098657 Homo sapi	c 763	1.0	166961	2	AC110425	AC110425 Homo sapi
c 691	1.0	158889	2	AC139188	AC139188 Rattus no	c 764	1.0	166961	2	AC110425	AC110425 Homo sapi
c 692	1.0	159115	2	AC006406	AC006406 Homo sapi	c 765	1.0	166961	2	AC110425	AC110425 Homo sapi
c 693	1.0	159219	2	AL590784	AL590784 Human DNA	c 766	1.0	166961	2	AC110425	AC110425 Homo sapi
c 694	1.0	159620	2	CR788294	CR788294 Danio rer	c 767	1.0	166961	2	AC110425	AC110425 Homo sapi
c 695	1.0	159636	2	AC135960	AC135960 Human DNA	c 768	1.0	166961	2	AC110425	AC110425 Homo sapi
c 696	1.0	159662	2	AC135960	AC135960 Human DNA	c 769	1.0	166961	2	AC110425	AC110425 Homo sapi
c 697	1.0	159875	2	AC148692	AC148692 Macaca mu	c 770	1.0	166961	2	AC110425	AC110425 Homo sapi
c 698	1.0	159908	2	AC069277	AC069277 Homo sapi	c 771	1.0	166961	2	AC110425	AC110425 Homo sapi
c 699	1.0	160087	2	AC007131	AC007131 Homo sapi	c 772	1.0	166961	2	AC110425	AC110425 Homo sapi
c 700	1.0	160255	10	AC127233	AC127233 Mus muscu	c 773	1.0	166961	2	AC110425	AC110425 Homo sapi
c 701	1.0	160338	3	AC099021	AC099021 Drosophi	c 774	1.0	166961	2	AC110425	AC110425 Homo sapi
c 702	1.0	160416	2	AC026181	AC026181 Homo sapi	c 775	1.0	166961	2	AC110425	AC110425 Homo sapi
c 703	1.0	160555	5	BX296516	BX296516 Zebrafish	c 776	1.0	166961	2	AC110425	AC110425 Homo sapi
c 704	1.0	160892	2	AC023910	AC023910 Homo sapi	c 777	1.0	166961	2	AC110425	AC110425 Homo sapi
c 705	1.0	160907	2	AC016642	AC016642 Homo sapi	c 778	1.0	166961	2	AC110425	AC110425 Homo sapi
c 706	1.0	161078	2	AP003500	AP003500 Homo sapi	c 779	1.0	166961	2	AC110425	AC110425 Homo sapi
c 707	1.0	161204	2	CNS01R11	AL162811 Human chr	c 780	1.0	166961	2	AC110425	AC110425 Homo sapi
c 708	1.0	161286	2	AC025120	AC025120 Homo sapi	c 781	1.0	166961	2	AC110425	AC110425 Homo sapi
c 709	1.0	161363	10	AL645535	AL645535 Mouse DNA	c 782	1.0	166961	2	AC110425	AC110425 Homo sapi
c 710	1.0	161397	2	AC090218	AC090218 Homo sapi	c 783	1.0	166961	2	AC110425	AC110425 Homo sapi
c 711	1.0	161489	2	AC025920	AC025920 Homo sapi	c 784	1.0	166961	2	AC110425	AC110425 Homo sapi
c 712	1.0	161545	10	AC132104	AC132104 Mus muscu	c 785	1.0	166961	2	AC110425	AC110425 Homo sapi
c 713	1.0	161694	2	CR391994	CR391994 Danio rer	c 786	1.0	166961	2	AC110425	AC110425 Homo sapi
c 714	1.0	162345	2	AC006415	AC006415 Papio anu	c 787	1.0	166961	2	AC110425	AC110425 Homo sapi
c 715	1.0	162345	3	AC006415	AC006415 Drosophi	c 788	1.0	166961	2	AC110425	AC110425 Homo sapi
c 716	1.0	162510	2	AC130337	AC130337 Homo sapi	c 789	1.0	166961	2	AC110425	AC110425 Homo sapi
c 717	1.0	162528	10	AL844263	AL844263 Mus muscu	c 790	1.0	166961	2	AC110425	AC110425 Homo sapi
c 718	1.0	162881	10	AL844264	AL844264 Mouse DNA	c 791	1.0	166961	2	AC110425	AC110425 Homo sapi
c 719	1.0	163102	2	AC093749	AC093749 Homo sapi	c 792	1.0	166961	2	AC110425	AC110425 Homo sapi
c 720	1.0	163121	2	AC110512	AC110512 Mus muscu	c 793	1.0	166961	2	AC110425	AC110425 Homo sapi
c 721	1.0	163321	2	AC126541	AC126541 Homo sapi	c 794	1.0	166961	2	AC110425	AC110425 Homo sapi
c 722	1.0	163400	2	AC010364	AC010364 Homo sapi	c 795	1.0	166961	2	AC110425	AC110425 Homo sapi
c 723	1.0	163876	2	AC016402	AC016402 Homo sapi	c 796	1.0	166961	2	AC110425	AC110425 Homo sapi
c 724	1.0	163980	2	AC009505	AC009505 Homo sapi	c 797	1.0	166961	2	AC110425	AC110425 Homo sapi
c 725	1.0	163900	2	AC079263	AC079263 Homo sapi	c 798	1.0	166961	2	AC110425	AC110425 Homo sapi
c 726	1.0	163943	10	AC122016	AC122016 Mus muscu	c 799	1.0	166961	2	AC110425	AC110425 Homo sapi
c 727	1.0	163978	5	BX119984	BX119984 Zebrafish	c 800	1.0	166961	2	AC110425	AC110425 Homo sapi
c 728	1.0	164021	2	AC102502	AC102502 Mus muscu	c 801	1.0	166961	2	AC110425	AC110425 Homo sapi
c 729	1.0	164055	2	AC110883	AC110883 Rattus no	c 802	1.0	166961	2	AC110425	AC110425 Homo sapi
c 730	1.0	164219	5	BX005205	BX005205 Zebrafish	c 803	1.0	166961	2	AC110425	AC110425 Homo sapi
c 731	1.0	164308	2	AC011280	AC011280 Homo sapi	c 804	1.0	166961	2	AC110425	AC110425 Homo sapi
c 732	1.0	164407	2	AC097229	AC097229 Sus scrof	c 805	1.0	166961	2	AC110425	AC110425 Homo sapi
c 733	1.0	164562	2	AC027471	AC027471 Homo sapi	c 806	1.0	166961	2	AC110425	AC110425 Homo sapi
c 734	1.0	164661	2	AC148524	AC148524 Homo sapi	c 807	1.0	166961	2	AC110425	AC110425 Homo sapi
c 735	1.0	164872	2	AC138080	AC138080 Homo sapi	c 808	1.0	166961	2	AC110425	AC110425 Homo sapi
c 736	1.0	165072	2	AC023993	AC023993 Homo sapi	c 809	1.0	166961	2	AC110425	AC110425 Homo sapi
c 737	1.0	165440	2	AC025035	AC025035 Homo sapi	c 810	1.0	166961	2	AC110425	AC110425 Homo sapi
c 738	1.0	165521	2	AC128282	AC128282 Rattus no	c 811	1.0	166961	2	AC110425	AC110425 Homo sapi
c 739	1.0	165609	2	AL536265	AL536265 Human DNA	c 812	1.0	166961	2	AC110425	AC110425 Homo sapi
c 740	1.0	165636	2	AC104110	AC104110 Homo sapi	c 813	1.0	166961	2	AC110425	AC110425 Homo sapi
c 741	1.0	166015	2	AC102794	AC102794 Mus muscu	c 814	1.0	166961	2	AC110425	AC110425 Homo sapi
c 742	1.0	166385	2	AC074340	AC074340 Homo sapi	c 815	1.0	166961	2	AC110425	AC110425 Homo sapi
c 743	1.0	167304	10	AL928678	AL928678 Mouse DNA	c 816	1.0	166961	2	AC110425	AC110425 Homo sapi
c 744	1.0	167357	2	AC055771	AC055771 Homo sapi	c 817	1.0	166961	2	AC110425	AC110425 Homo sapi
c 745	1.0	167710	2	AC109891	AC109891 Rattus no	c 818	1.0	166961	2	AC110425	AC110425 Homo sapi
c 746	1.0	167946	2	AC083806	AC083806 Homo sapi	c 819	1.0	166961	2	AC110425	AC110425 Homo sapi
c 747	1.0	167946	2	AC116861	AC116861 Mus muscu	c 820	1.0	166961	2	AC110425	AC110425 Homo sapi
c 748	1.0	168144	2	CR792456	CR792456 Danio rer	c 821	1.0	166961	2	AC110425	AC110425 Homo sapi
c 749	1.0	168144	2	AL159171	AL159171 Human DNA	c 822	1.0	166961	2	AC110425	AC110425 Homo sapi
	1.0	168344	10	AC126028	AC126028 Mus muscu						

823	19	1.0	182033	5	EX323544	896	19	1.0	197729	10	AL663056	AL663056	Mouse DNA
C 824	19	1.0	182178	9	AC074198	897	19	1.0	197831	10	AC117224	AC117224	Mus muscu
C 825	19	1.0	182416	2	AC023044	898	19	1.0	197871	10	AC134462	AC134462	Mus muscu
C 826	19	1.0	182740	9	AC113418	C 899	19	1.0	197959	2	AC134688	AC134688	Mus muscu
C 827	19	1.0	182839	2	AC022619	C 900	19	1.0	198001	2	AC148323	AC148323	Mus muscu
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Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Datchenko, L., Martusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
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Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, B. D.,
Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 15899-15903 (2002)

Journal: *Journal of the National Institutes of Health*

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	On Dec 16 2003 this sequence version replaced ci.21543251

Tissue Procurement: Miklos Palukovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

http://www.systemsbiology.org
contact: amadan@systemsbiology.org

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNt at: <http://image.lnl.gov>

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OY 784 TCTCAGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 843
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OY 904 CAGGAGCTGATTCATTCAGCCGAGAAATAGATGAAATGAAATGAAATGAAATGAAATG 963
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OY 964 TCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1023
DB 961 TCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
OY 1024 CTGGGCTGCTGCTATTCATGCTGAGAGAAATCTGATATTAACCCGACGACGACGACG 1083
DB 1021 CTGGGCTGCTGCTATTCATGCTGAGAGAAATCTGATATTAACCCGACGACGACGACG 1080
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DB 1141 GGGGACACATGCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
OY 1204 CACTCAGAGGCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1263
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RESULT 3
BD268022 1912 bp DNA linear PAT 17-JUL-2003
LOCUS Proteases and associated proteins.
DEFINITION BD268022
ACCESSION BD268022.1 GI:33077790
VERSION JP 2002522081-A/10.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1912)
AUTHORS Bandman,O., Hillman,J.L., Baughn,M.R., Azimzai,Y., Guegler,K.J., Corley,N.C., Yue,H., Tang,T.Y., Reddy,R., Patterson,C., Young,J.A., Shih,L.L. and Lu,D.A.M.
TITLE Proteases and associated proteins
JOURNAL Patent: JP 2002522081-A 10 23-JUL-2002;
COMMENT INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002522081-A/10
PD 23-JUL-2002
PR 06-AUG-1999 JP 2000565144
PR 10-AUG-1998 US 60/096114,11-FEB-1999 US 60/119768 PI
OLGA BANDMAN,JENNIFER L HILLMAN,MARIAH R BAUGHN,YALDA AZIMZAI, PI
KARL J GUEGLER,NEIL C CORLEY,HENRY YUE,TOM Y TANG,ROOPA REDDY, PI
CHANDRA PATERSON,JANICE AU YOUNG,LEO L SHIH,DYUNG AINA M LU PC
CI2N15/09,A61K38/00,A61K45/00,A61P37/00,A61P43/00,C07K16/40, PC
CI2N1/15,
PC CI2N1/19,CI2N1/21,CI2N5/10,CI2N9/48,CI2P21/08,CI2Q1/68,CI2N15/
PC 00,CI2N5/00,
PC A61K37/02
CC Incyte Clone No: 1393301
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FT source 1.1912
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FEATURES
source
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 1817 TTGGGTTGAGCAACATGCTCCAGAGAGGCGCAGGTGGAGCTGGCCCTTAAAGAA 1876
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RESULT 4
 LOCUS BD192303 1899 bp DNA linear PAT 17-JUL-2003
 DEFINITION Secreted proteins and polynucleotides encoding them.
 ACCESSION BD192303
 VERSION BD192303.1 GI:33002042
 KEYWORDS JP 2002513294-A/6.
 SOURCE unclassified
 ORGANISM unclassified
 REFERENCE 1 (bases 1 to 1899)
 AUTHORS Jacobs,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Trenc,M.,
 TITLE Spaulding,V., Agostino,M.J., Howes,S.H. and Fechtel,K.,
 JOURNAL Secreted proteins and polynucleotides encoding them
 Patient: JP 2002513294-A 6 08-MAY-2002;
 GENETICS INSTITUTE INC
 PN JP 2002513294-A/6
 PD 08-MAY-2002
 PF 18-JUN-1998 JP 199504681
 PR 19-JUN-1997 US 08/878715.17-JUN-1998 US 09/098568 PI
 KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
 MAURICE TREACY
 PI VIKKI SPAULDING, MICHAEL J AGOSTINO, STEVEN H HOWES, KIM FECHTEL
 PC C07K1/00, C07H21/02, A61K39/00, C12N1/20
 CC Strandedness: Double;
 Topology: Linear;

FEATURES FH Key Location/Qualifiers.
 Source 1..1899
 /organism="unclassified"
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Query Match 78.8%; Score 1494; DB 6; Length 1899;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Qy 191 CACTGTGACTCAGCTCTGAAAGGAGAGACTACCTGCTGCTGCTGCTGCTGCTGCTGCT 250
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 Qy 251 GCGGAAATCCCACTGCTGCAAGTGAACCAATATGAAACCAAGCTTATGTCGAGATG 310
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 Qy 311 GTGCTGTGCTGCTCAACTCTCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
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Db	965	GGAGAAACCAAAACCCTGGCAGCCCTCTGACAGCTGCCCAACAGAGGCCCTTGCTGATGC	1022
Qy	1031	TGTGCTATTTCGATCGTGGAGAAATACCTGATCATTAACCCCAAGGCCCTGGAAGT	1090
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Qy	1091	ACATGAGAGAGAGATCCTTGATTTGGGAAAGTCGTGTCAGACCTTGGAGGCCGAC	1156
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Qy	1151	ACATGCTACCTGTGCTCTCTGTGACCTTCTGCTCCCTTGAAGCTGAGCAGTCCACTAG	1210
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Qy	1211	AGGCCAGCTTGACGCGCAACATGCGACACCTCCCAAGACTCCCTTGTCAAGCCCT	1270
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Qy	1331	TTTACGGGCTGGAATTTGTACGGTGGGCTCCACATATGACTTCTGAGTCCCGGCTTGCA	1390
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Qy	1391	CGAAAGCTGTGAAGATGTCGAGCTCTCGGATGGCTCCAGACTGATCTCTTAGCTTCC	1450
Db	1385	CGAAAGCTGTGAAGATGTCGAGCTCTCGGATGGCTCCAGACTGATCTCTTAGCTTCC	1444
Qy	1451	AGGATGGGGATTTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCAAACTACT	1510
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Qy	1571	GATGCTGCGAATGAGACTTACAGTGGCGCTGAGCC	1606
Db	1565	GATGCTGCGAATGAGACTTACAGTGGCGCTGAGCC	1600
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DEFINITION	95 human secretory proteins.		linear
ACCESSION	BD136402		
VERSION	BD136402.1		
KEYWORDS	JP 2002506627-A/89.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1892)		
TITLE	Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P., Soppel,D.R., Wei,Y.F., Endress,G.A., Dunn,R.D., Kyaw,H., Ebner,R., Latleir,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.		
JOURNAL	95 human secretory proteins Patent: JP 2002506627-A 89 05-MAR-2002; HUMAN GENOME SCIENCES INC		
COMMENT	OS Homo sapiens (human) PN JP 2002506627-A/89 PD 05-MAR-2002 PF 18-MAR-1999 JP 2000536733 PR 19-MAR-1998 US 60/078566,19-MAR-1998 US 60/078576 PR 19-MAR-1998 US 60/078573,19-MAR-1998 US 60/078574 PR 19-MAR-1998 US 60/078579,19-MAR-1998 US 60/078578 PR		

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ACCESSION	CQ722423		
VERSION	CQ722423.1	GI:42283280	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.		
FEATURES	Kits, such as nucleic acid arrays, comprising a majority of		
source	humanexons or transcripts, for detecting expression and other uses		
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Matches 769;	Conservative 0;	Mismatches 1;	Indels 0;
		Gaps 0;	
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QY	848	CTTTTGCTCCCCGGGTGAGAAAGTGAAGTCTCTCTATGATATGAGAAATCAG	907
Db	416	CTTTTGCTCCCCGGGTGAGAAAGTGAAGTCTCTCTATGATATGAGAAATCAG	907
QY	908	AGCTCATTCATTAAGCCCAAGAAATGATGAATGAATATATGATGAACTCT	967
Db	476	AGCTCATTCATTAAGCCCAAGAAATGATGAATGAATATATGATGAACTCT	967
QY	968	ACTGAGAAACCAAAACCTTGAGCTTCTCAGCTGCGCCCAAGAGCTTGTCTG	1027
Db	536	ACTGAGAAACCAAAACCTTGAGCTTCTCAGCTGCGCCCAAGAGCTTGTCTG	1027
QY	1028	TGCTGTGCTATTCATTCGTGAGAAATACCTGATATATACCCCAAGAGCTTGTG	595
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Db	656	AGTACATGAGAGAGAAATCTTGGTTTCGGAAGTGGTCTGTGACAGCTTGGGGC	1147
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QY	1268	CTTGTGCTTCCCGAGGCTTTCATGAGCAACAGAGTGAAGGCTCCAGAAATAGGCC	1327
Db	836	CTTGTGCTTCCCGAGGCTTTCATGAGCAACAGAGTGAAGGCTCCAGAAATAGGCC	1327
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RESULT 7
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LOCUS Extended cDNA of secretory protein.
DEFINITION BD139445
ACCESSION BD139445 GI:23234390
VERSION JP 2002508182-A/197.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 964)
Bougueleret, L., Duclet, A. and Edwards, J. B. D. M.
Extended cDNA of secretory protein
Patent: JP 2002508182-A 197 19-MAR-2002;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002508182-A/197
PD 19-MAR-2002 JP 2000539136
PF 17-DEC-1998 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET, AYMERIC DUCLET, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
Von Heijne matrix
CC score 8.5
CC seq LKVLPLPLAPAA/OD
FH Key Location/Qualifiers
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FT sig_peptide 21..95
FT polyA_signal 921..926
FT polyA_site 953..963.
FT Location/Qualifiers
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Best Local Similarity 99.3%; Pred. No. 2,7e-295;
Matches 948; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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Db 2 GGGCGGATCTTCCGGCCATGAGAAAGCCAGCGGCTGCTTCCCTCCCTCAGTCCGAA 61
QY 90 GGTGCTGCTCTGCTCTGCTGAGCACTGCGGAGCCAGAGATTGACTCAGGCCCCCACTCC 149
Db 62 GGTGCTGCTCTGCTCTGCTGAGCACTGCGGAGCCAGAGATTGACTCAGGCCCCCACTCC 121
QY 150 AGGACAGCCCTCTCTCTCCATACGGAATACGAGAGCTTCTTGGCACTGCTGACTCCAACTCG 209
Db 122 AGGACAGCCCTCTCTCTCCATACGGAATACGAGAGCTTCTTGGCACTGCTGACTCCAACTCG 181
QY 210 GAAGCAGAGACTACTGCGGTCTCGGTGCAACCCAGCGCTGCGGAATCCACACTCGT 269

Db 182 GAAAGCAGAACTACTGCGCTCCGTCCGTCACCCAGCGCTGCCGGAATCCACACTCGT 241
QY 270 CCAAGTGAACCAATATGAAAACCAAGGCTTAGGCGCGAATGAGTGTCTGCTCAACT 329
Db 242 CCAAGTGAACCAATATGAAAACCAAGGCTTAGGCGCGAATGAGTGTCTGCTCAACT 301
QY 330 CCCTATGCTCTGCTGTTGAGTCTTCTGCGCAGTTCACTCAGTACCGTTGCTCAACA 389
Db 302 CCCTATGCTCTGCTGTTGAGTCTTCTGCGCAGTTCACTCAGTACCGTTGCTCAACA 361
QY 390 CGTCTATATGCAAGAGAGTCTGTGTCCAGCCAGTCTATTTCTCTACCTTAAC 449
Db 362 CGTCTATATGCAAGAGAGTCTGTGTCCAGCCAGTCTATTTCTCTACCTTAAC 421
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QY 629 AGCACAAGCAG 688
Db 602 AGCACAAGCAG 661
QY 689 AAGAGGGGAG 748
Db 662 AAGAGGGGAG 721
QY 749 AAGAGAGGGAG 808
Db 722 AAGAGAGGGAG 781
QY 809 CCAAGTTTCACTGATCTATCTTCTTCAACCTTCTCTTTGCTCCCGGGTACAG 868
Db 782 CCAAGTTTCACTGATCTATCTTCTTCAACCTTCTCTTTGCTCCCGGGTACAG 841
QY 869 AAGTAGAGTCTACTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 928
Db 842 AAGTAGAGTCTACTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 901
QY 929 AATATGATGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 983
Db 902 AATATGATGAATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 956
RESULT 8
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LOCUS Homo sapiens 12 BAC RP11-433J6 (Rosewell) Park Cancer Institute Human
DEFINITION BAC library complete sequence.
ACCESSION AC135892
VERSION AC135892.1 GI:24371346
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 56520)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C.,
Alshrocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbieri, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burck, P., Burkett, C., Butrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C.,
Clelland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 56520)
Morley, K.C.
Submitted (25-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMaker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST ESR and cDNA sequences. Genes demonstrate at least < 1e-34 to the flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 clones with no ambiguities or 2 chemistries with a minimum of 2 a region and 3 reads with no ambiguities. If the sequence quality for annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality

standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at http://www.hgsc.bcm.tmc.edu:8088/quality_info/genbank_annotation.html.

FEATURES

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Location/Qualifiers

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/db_xref="taxon:9606"

/chromosome="12"

/clone="RP11-433J6"

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/rpt_family="AluX"

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9819..10121

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Best Local Similarity 100.0%; Pred. No. 3.2e-262;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 642 GCAAGAGTGAAGCAAGGAGGAGCCGACACAAAGCAAGCAAGAGGAGGAGCAAA 701
DB 44570 GCAAGAGTGAAGCAAGGAGGAGCCGACACAAAGCAAGCAAGAGGAGGAGCAAA 44511
QY 702 ACGGAAGAGCAAGAGAGAGCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
DB 44510 ACGGAAGAGCAAGAGAGAGCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 44451
QY 762 TAAGGAGGAGGAGGAGGCTGTCTCAGCTGAGAGCAAGCTCAGAGCCCAAGTTTCACTC 821
DB 44450 TAAGGAGGAGGAGGAGGCTGTCTCAGCTGAGAGCAAGCTCAGAGCCCAAGTTTCACTC 44391
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DB 44390 TGAATCTATCTTCTTAACCTTCTCTTCTGCTCCCGGGTACGAGAGTGAAGTCTAC 44331
QY 882 TCTATGATTAATGAGAAACATCCAGAGCTCATTCATCAGCCCAAGAAATAGATGAAT 941
DB 44330 TCTATGATTAATGAGAAACATCCAGAGCTCATTCATCAGCCCAAGAAATAGATGAAT 44271
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ACCESSION  AC079387
VERSION    AC006087
KEYWORDS  HTG; HTGS PHASE1.
SOURCE     Homo sapiens (human)
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            Muzny,D.M., Adams,C., Bailey,M., Barabara,J., Blankenburg,K.,
            Bodora,B., Bouck,J., Bowie,S., Brooks,C., Buhay,A., Bunac,C.,
            Burdett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
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            Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
            Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
            Guevara,M., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
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            Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
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            Tabot,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M.,
            Wallington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
            Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
            Gibbs,R.
            Direct Submission
            Unpublished
            2 (bases 1 to 245880)
            Worley,K.C.
            Reference
            Submitted (01-SEP-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On or before Sep 1, 2000 this sequence version replaced gi:4589937,
            gi:4926836, gi:4589936.
            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
            Center project name: J-31
            Center clone name: RP4-761J14, RP11-433J6
            ----- Summary Statistics
            Sequencing vector: M13; L08821
            Chemistry: Dye-terminator Big Dye; 92% of reads
            Chemistry: Dye-terminator Big Dye; 7% of reads
            Assembly program: Phrap; version 0.990329
            Consensus quality: 214565 bases at least Q40
            Consensus quality: 230283 bases at least Q30
            Consensus quality: 240000 bases at least Q20
            Estimated insert size: 29807; agarose-1p estimation
            Quality coverage: 0x in Q20 bases; agarose-1p estimation
            -----
            * NOTE: Estimated insert size may differ from sequence length
            * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
            * NOTE: This is a "working draft" sequence. It currently
            * consists of 42 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 27068: contig of 27068 bp in length
            * 27069 27168: gap of unknown length

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* 240851 240950: gap of unknown length
* 240951 242140: contig of 1190 bp in length
* 242141 242240: gap of unknown length
* 242241 243504: contig of 1264 bp in length
* 243505 243604: gap of unknown length
* 243605 244749: contig of 1145 bp in length
* 244750 244849: gap of unknown length
* 244850 245880: contig of 1031 bp in length.

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Best Local Similarity	100.0%	Pred. No. 2.9e-262;		
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522 AGTGCAGGAAGCCAGACTCTTCCAGGCCCTCGGCTCAGAGGCTCAGCAACAACGTGGAAGA 581
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65632 GCACGAGTGGAGCA CAGGCAAGACCGACA CAAAGAACACACACGAGAAAGGGGCGAAG 65573

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65512 TAAGGAGGACGGAGAGCGTCTGTCTCAAGCTGCAGAACAAGATCTCAGAGCCCAATTTCATGC

822 TGAATCTAATCTTAAACCTTCTCTTTTGTGCTCCCGGATACGAAGAAGTACTTAC 881
65452 TGAATCTAATCTTAAACCTTCTCTTTTGTGCTCCCGGATACGAAGAAGTACTTAC 65393

[illegible]

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RESULT 10

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U00002	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00003	5S rRNA	5S rRNA	120	3.9	5.5	1
U00004	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00005	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00006	5S rRNA	5S rRNA	120	3.9	5.5	1
U00007	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00008	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00009	5S rRNA	5S rRNA	120	3.9	5.5	1
U00010	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00011	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00012	5S rRNA	5S rRNA	120	3.9	5.5	1
U00013	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00014	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00015	5S rRNA	5S rRNA	120	3.9	5.5	1
U00016	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00017	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00018	5S rRNA	5S rRNA	120	3.9	5.5	1
U00019	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00020	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00021	5S rRNA	5S rRNA	120	3.9	5.5	1
U00022	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00023	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00024	5S rRNA	5S rRNA	120	3.9	5.5	1
U00025	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00026	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00027	5S rRNA	5S rRNA	120	3.9	5.5	1
U00028	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00029	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00030	5S rRNA	5S rRNA	120	3.9	5.5	1
U00031	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00032	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00033	5S rRNA	5S rRNA	120	3.9	5.5	1
U00034	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00035	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00036	5S rRNA	5S rRNA	120	3.9	5.5	1
U00037	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00038	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00039	5S rRNA	5S rRNA	120	3.9	5.5	1
U00040	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00041	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00042	5S rRNA	5S rRNA	120	3.9	5.5	1
U00043	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00044	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00045	5S rRNA	5S rRNA	120	3.9	5.5	1
U00046	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00047	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00048	5S rRNA	5S rRNA	120	3.9	5.5	1
U00049	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00050	23S rRNA	23S rRNA	2304	78.04	5.5	1
U00051	5S rRNA	5S rRNA	120	3.9	5.5	1
U00052	16S rRNA	16S rRNA	1542	32.07	5.5	1
U00053	23S rRNA	23S rRNA	2304	78		

KEYWORDS: FilicDNA, Homo sapiens (human), Homo sapiens, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Metazoa.

REFERENCE
AUTHORS
I (Bases 1 to 516)
Weesner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J.,
Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Thaising, B.,
Geisels, S., Allen, M., Underwood, K., Channell, J., Bertram, P.,
Giles, J., and others. 1997. *Journal of Virology* 71: 1000-1008.

Full Clone Sequencing of the Longest Available Member from Each

Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 516)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY: Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

NOTE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

SIMILARITY INFORMATION:
similar to Sus scrofa domestica protein A54424 (PID:g1082952)
acrosomal protein sp32 precursor - pig (fragment)

FEATURES
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ORIGIN
Query Match 17.9%; Score 339; DB 9; Length 516;
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Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1557 GGTGTCCTCCGATAGATGCTGAGATGAGACTTACAGTGCCTGAGCCCTGGCAAAAG 1616
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1617 TGAAGAGCTTGTGCTTGCATGAGCCAGAGATTACAGCACTTGAAGCCAGTTGCG 1676
237 TGAAGAGCTTGTGCTTGCATGAGCCAGAGATTACAGCACTTGAAGCCAGTTGCG 296
1677 ATGAGCTGGAGCTTATTTGCGCCCAACAGCCCAACCTGCGCCAGTTCTTATTTGTTT 1736
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357 TGAAGCCCACTTCTTCAAGGCTGCGCTTCTGGGTCTGTTACTCGGCCCTTACAT 416
1797 TTCTCTTGGTTGAGCAACAGTCCAGAGAGGCGCAGTGGAGAGTGGCCCTCTTAA 1856
417 TTCTCTTGGTTGAGCAACAGTCCAGAGAGGCGCAGTGGAGAGTGGCCCTCTTAA 476

QY 1857 AGATGACTTTACATAAATGTTGATCTTCAAAAAA 1895
Db 477 AAGATGACTTTACATAAATGTTGATCTTCAAAAAA 515

RESULT 11
BD060281 308 bp DNA linear PAT 27-AUG-2002
LOCUS Secretd expressed sequence tags (ESTs).
DEFINITION BD060281
ACCESSION BD060281.1 GI:22605887
VERSION BD060281.1
KEYWORDS JP 2001518793-A/641.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 308)
REFERENCE
AUTHORS Jacobs, K., McCoy, J.M., Lavallie, E.R., Racine, L.A., Werberg, D., Treacy, M., Spaulding, V. and Agostino, M.J.
TITLE Secretd expressed sequence tags (ESTs)
JOURNAL Patent: JP 2001518793-A 641 16-Oct-2001;
GENETICS INSTITUTE INC
PN JP 2001518793-A/641
PD 16-Oct-2001
PF 10-Apr-1998 JP 1998543070
PR 10-Apr-1997 US 08/837312
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACINE, PI DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC
double;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 414 GTGTCCGACGAGTCTTATTTCTACCTTACACTTCAAGAGATGAGCTTCAGC 473
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QY 474 TGAAGTCAACCCAGCAACGATGACCTTCCCATCTTCAACCTTCAAGAGATGAGAGG 533
Db 82 TGAAGTCAACCCAGCAACGATGACCTTCCCATCTTCAACCTTCAAGAGATGAGAGG 141
QY 534 CCAAGCTTCCAGCTGAGCTGAGAGGCTCAGCAACAAGTGAAGAGCTCTTACATC 593
Db 142 CCAAGCTTCCAGCTGAGCTGAGAGGCTCAGCAACAAGTGAAGAGCTCTTACATC 201
QY 594 CTCCTTGTCTTGGAGGCGCAGAGCAAGGCCAGAGCAACAAGCAGAGCAGAGTGA 653
Db 202 CTCCTTGTCTTGGAGGCGCAGAGCAAGGCCAGAGCAACAAGCAGAGCAGAGTGA 261
QY 654 GCAAGGCAAGAGCCGACACAAAGAAACAAGCAGAGAGG 694
Db 262 GCAAGGCAAGAGCCGACACAAAGAAACAAGCAGAGAGG 302

RESULT 12
BD179252 507 bp DNA linear PAT 16-APR-2003
LOCUS Cancer associated gene.
DEFINITION BD179252
ACCESSION BD179252.1 GI:30016521
VERSION

KEYWORDS WO 02083899-A/230.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Yoshioka, Y., Okamoto, S., Oura, T., Junichi, Mineno, Asada, K., Kato, I., Inoue, H. and Mori, M.
TITLE Cancer associated gene
JOURNAL Patent: WO 02083899-A 230 24-OCT-2002; TAKARA SHUZO CO LTD, YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
COMMENT OS Homo sapiens (human)
PN WO 02083899-A/230
PD 24-OCT-2002
PF 28-MAR-2002 WO 2002JP003038
PR 10-APR-2001 JP 01P 112039, 21-SEP-2001 JP 01P 290193 PI
YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
MINENO, KIYOZO ASADA,
PI IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI
PC C12N15/12, C07K14/82, C07K16/32, C12P21/08, C12Q1/68, A61K39/395,
PC A61K48/00,
PC A61P35/00, G01N33/50, G01N33/53
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FT source
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QY 1616 GTGAGAGAGCTTGTGCTTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 235
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DB 296 GATGAGCTGGCTGATTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 295
QY 1736 TTGAGAGCCCATGCTTTCAGAGCTGGCTTCGAGTCTGTAAGCCCTGGCAAAA 1735
DB 356 TTGAGAGCCCATGCTTTCAGAGCTGGCTTCGAGTCTGTAAGCCCTGGCAAAA 355
QY 1796 TTTCCTGGGTTGGAGCAACAGTCCAGAGAGGCGCAAGCTGGAGCTGGCTGGCTTCA 415
DB 416 TTTCCTGGGTTGGAGCAACAGTCCAGAGAGGCGCAAGCTGGAGCTGGCTGGCTTCA 475
QY 1856 AAAAGTACTTTACATAAATGTTGATCTTC 1886
DB 476 AAAAGTACTTTACATAAATGTTGATCTTC 506
RESULT 13
BD179034
LOCUS BD179034 522 bp DNA linear PAT 16-APR-2003
DEFINITION Cancer associated gene.
ACCESSION BD179034
VERSION BD179034.1 GI:30016302
KEYWORDS WO 02083899-A/12.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Yoshioka, Y., Okamoto, S., Oura, T., Junichi, Mineno, Asada, K., Kato, I., Inoue, H. and Mori, M.
TITLE Cancer associated gene
JOURNAL Patent: WO 02083899-A 12 24-OCT-2002; TAKARA SHUZO CO LTD, YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
COMMENT OS Homo sapiens (human)
PN WO 02083899-A/12
PD 24-OCT-2002
PF 28-MAR-2002 WO 2002JP003038
PR 10-APR-2001 JP 01P 112039, 21-SEP-2001 JP 01P 290193 PI
YOSHIE YOSHIKAWA, SACHIKO OKAMOTO, TOMONORI OURA, JUNICHI PI
MINENO, KIYOZO ASADA,
PI IKUNOSHIN KATO, HIROSHI INOUE, MASAKI MORI
PC C12N15/12, C07K14/82, C07K16/32, C12P21/08, C12Q1/68, A61K39/395,
PC A61K48/00,
PC A61P35/00, G01N33/50, G01N33/53
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FT source
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Best Local Similarity 99.7%; Pred. No. 1.2e-150;
Matches 330; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1556 AGGTGTCCTGAGATGATGTCGAGATGAGACTTACAGTGGCTGAGCCCTGGCAAAA 1615
DB 176 AGGTGTCCTGAGATGATGTCGAGATGAGACTTACAGTGGCTGAGCCCTGGCAAAA 235
QY 1616 GTGAGAGAGCTTGTGCTTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 235
DB 236 GTGAGAGAGCTTGTGCTTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 235
QY 1676 GATGAGCTGGCTGATTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 1675
DB 296 GATGAGCTGGCTGATTCGATGAGAGCCAGAGATTCAGACCTTGAAGCCCTGGCAAAA 295
QY 1736 TTGAGAGCCCATGCTTTCAGAGCTGGCTTCGAGTCTGTAAGCCCTGGCAAAA 1735
DB 356 TTGAGAGCCCATGCTTTCAGAGCTGGCTTCGAGTCTGTAAGCCCTGGCAAAA 355
QY 1796 TTTCCTGGGTTGGAGCAACAGTCCAGAGAGGCGCAAGCTGGAGCTGGCTGGCTTCA 415
DB 416 TTTCCTGGGTTGGAGCAACAGTCCAGAGAGGCGCAAGCTGGAGCTGGCTGGCTTCA 475
QY 1856 AAAAGTACTTTACATAAATGTTGATCTTC 1886
DB 476 AAAAGTACTTTACATAAATGTTGATCTTC 506
RESULT 14
G23540/c
LOCUS G23540/c 391 bp DNA linear STS 31-MAY-1996
DEFINITION human STS WI-30262, sequence tagged site.
ACCESSION G23540
VERSION G23540.1 GI:1343866
KEYWORDS STS; STS sequence, primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 391)

AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
JOURNAL Mapped STS
COMMENT Unpublished (1995)

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: AGTCATCTTTAAGAGAGGCG
Primer B: AGACCCATTGCTTCAGC
STS size: 126
PCR Profile:

Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:

Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/uI
Total Vol: 20 uI

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

FEATURES
source Derived from dbEST (genbank accession H30251).
Location/Qualifiers
1..391

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="83.0 cR from top of Chr12 linkage group"
STS
primer_bind 23..43
primer_bind complement(130..148)
ORIGIN

Query Match 7.9%; Score 149; DB 11; Length 391;
Best Local Similarity 99.5%; Pred. No. 3.1e-74;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1641 CCAGGAGTTAGACACTTGAAGCCAGTTGGATGAGTGGCGTTATTCGCCA 1700
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QY 1701 CACCCAGCCCACTGCGCAAGTCTCTATGTTTGAAGACCCATTGCTTCAGGCTG 1760
DB 186 CACCCAGCCCACTGCGCAAGTCTCTATGTTTGAAGACCCATTGCTTCAGGCTG 127
QY 1761 CCCCTTCTGGGTCTGTACTCGGCCCTTACTCATTCTCTGGGTTGAGACAAGTCC 1820
DB 126 CCCCTTCTGGGTCTGTACTCGGCCCTTACTCATTCTCTGGGTTGAGACAAGTCC 67
QY 1821 CAGAGAGGGCCAGCGTGGGA 1840
DB 66 CAGAGAGGGCCAGCGTGGGA 47

RESULT 15
AX968632
LOCUS AX968632 128 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 60 from Patent EP1378571.

ACCESSION AX968632
VERSION AX968632.1 GI:40975063
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Dumas Milne Edwards,J.B., Duclert,A. and Lacroix,B.
TITLE 5' ESTs for secreted proteins expressed in various tissues
JOURNAL Patent: EP 1378571-A 60 07-JUN-2004;
GENSET (FR)

FEATURES
source Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GGGCGATCTTCTCCGGCATGAGAGCGCGCTGCTTCCTTCCTCACTCGAA 61
QY 90 GGTGCTGCTCTGCTGCTGCACTGCGCAGCCAGATTCAGTCCAGGCC 141
DB 62 GGTGCTGCTCTGCTGCTGCACTGCGCAGCCAGATTCAGTCCAGGCC 113

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GenCore version 5.1.6
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Scoring table: OLIGO_NUC
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Searched: 5401638 seqs, 2966923429 residues

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and is derived by analysis of the total score distribution.

SUMMARIES

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1	1895	100.0	1895	17	US-10-148-641A-23
2	1886	99.5	1886	16	US-10-262-666-41
3	1886	99.5	1886	17	US-10-085-117-53
4	1632	86.1	1632	17	US-10-085-117-53
5	1494	80.7	1494	18	US-10-719-993-124
6	1494	78.8	1494	10	US-09-746-783-77
7	1284	67.8	1284	10	US-09-397-945-90
8	1284	67.8	1284	17	US-10-653-595-90
9	1173	61.9	1671	17	US-10-296-115-693
10	528	27.9	964	11	US-09-978-360A-262
11	471	24.9	21347	18	US-10-719-993-6794

12	471	24.9	29346	17	US-10-085-117-52	Sequence 52, Appl
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14	328	17.3	24923	18	US-10-719-993-7043	Sequence 7043, Ap
15	307	16.2	474	10	US-09-918-995-36471	Sequence 36471, A
16	281	14.8	308	13	US-10-040-739-641	Sequence 641, Ap
17	281	14.8	28953	18	US-10-719-993-6811	Sequence 6811, Ap
18	280	14.8	507	18	US-10-474-495-230	Sequence 230, App
19	280	14.8	522	18	US-10-474-495-12	Sequence 12, Appl
20	150	7.9	201	18	US-10-719-993-2295	Sequence 2295, Ap
21	150	7.9	201	18	US-10-719-993-2296	Sequence 2296, Ap
22	147	7.8	201	18	US-10-719-993-2297	Sequence 2297, Ap
23	147	7.8	201	18	US-10-719-993-2298	Sequence 2298, Ap
24	104	5.5	157	18	US-10-719-993-2294	Sequence 2294, Ap
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26	104	5.5	201	18	US-10-719-993-17827	Sequence 17827, A
27	100	5.3	201	18	US-10-719-993-15236	Sequence 15236, A
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29	97	5.0	201	18	US-10-719-993-15238	Sequence 15238, A
30	93	4.9	201	18	US-10-719-993-15250	Sequence 15250, A
31	88	4.6	201	18	US-10-719-993-15239	Sequence 15239, A
32	82	4.3	201	18	US-10-719-993-15240	Sequence 15240, A
33	60	3.2	60	10	US-09-908-975-22261	Sequence 22261, A
34	51	2.7	201	18	US-10-719-993-15251	Sequence 15251, A
35	49	2.6	201	18	US-10-719-993-15235	Sequence 15235, A
36	46	2.4	1623	17	US-10-085-117-51	Sequence 51, Appl
37	46	2.4	1840	17	US-10-085-117-50	Sequence 50, Appl
38	46	2.4	36211	17	US-10-085-117-49	Sequence 49, Appl
39	40	2.1	201	18	US-10-719-993-15252	Sequence 15252, A
40	27	1.4	29	10	US-09-746-783-92	Sequence 92, Appl
41	25	1.3	25	19	US-10-719-900-332039	Sequence 32039, A
42	23	1.2	23	17	US-10-148-641A-34	Sequence 34, Appl
43	23	1.2	25	19	US-10-719-900-912511	Sequence 912511, A
44	23	1.2	345	14	US-10-043-648-133	Sequence 133, App
45	22	1.1	22	17	US-10-148-641A-31	Sequence 31, Appl
46	21	1.1	21	17	US-10-148-641A-30	Sequence 30, Appl
47	20	1.1	20	16	US-10-262-666-27	Sequence 27, Appl
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49	20	1.1	20	17	US-10-148-641A-27	Sequence 27, Appl
50	20	1.1	20	17	US-10-148-641A-28	Sequence 28, Appl
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52	20	1.1	20	17	US-10-148-641A-32	Sequence 32, Appl
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71	20	1.1	7177	13	US-10-033-026-7	Sequence 7, Appl
72	20	1.1	7177	18	US-10-736-883-33	Sequence 33, Appl
73	20	1.1	7363	17	US-10-375-253-11	Sequence 11, Appl
74	20	1.1	7363	18	US-10-723-860-5192	Sequence 5192, Ap
75	20	1.1	7364	9	US-09-954-456-1179	Sequence 1179, Ap
76	20	1.1	7364	13	US-10-033-026-5	Sequence 5, Appl
77	20	1.1	7364	18	US-10-736-883-31	Sequence 31, Appl
78	20	1.1	7376	13	US-10-033-026-3	Sequence 3, Appl
79	20	1.1	35956	15	US-10-017-161-761	Sequence 761, App
80	20	1.1	77334	13	US-10-087-192-343	Sequence 343, App
81	20	1.1	198073	13	US-10-087-192-343	Sequence 682, App
82	20	1.0	19	17	US-10-148-641A-33	Sequence 33, Appl
83	19	1.0	19	18	US-10-719-993-55162	Sequence 55162, A
84	19	1.0	201	18	US-10-719-993-15237	Sequence 15237, A

85	19	1.0	313	18	US-10-425-115-33221	Sequence 33221, A
86	19	1.0	334	9	US-09-960-352-2620	Sequence 2620, App
87	19	1.0	440	9	US-09-560-863-864	Sequence 864, App
88	19	1.0	472	17	US-10-242-535A-42992	Sequence 42992, A
89	19	1.0	472	17	US-10-085-783A-42992	Sequence 42992, A
90	19	1.0	538	18	US-10-425-115-182049	Sequence 182049, A
91	19	1.0	561	13	US-10-027-632-186996	Sequence 186996, A
92	19	1.0	561	17	US-10-027-632-186996	Sequence 186996, A
93	19	1.0	588	18	US-10-437-632-294	Sequence 294, App
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95	19	1.0	729	18	US-10-767-701-1233	Sequence 1233, App
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97	19	1.0	735	17	US-10-027-632-110125	Sequence 110125, A
98	19	1.0	963	15	US-10-204-887-71	Sequence 71, App
99	19	1.0	1665	17	US-10-082-122A-32579	Sequence 32579, A
100	19	1.0	1833	17	US-10-282-122A-32579	Sequence 32579, A
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102	19	1.0	2139	17	US-10-283-842A-3447	Sequence 3447, App
103	19	1.0	2202	13	US-10-027-632-102111	Sequence 102111, A
104	19	1.0	2202	17	US-10-027-632-102111	Sequence 102111, A
105	19	1.0	3080	17	US-10-378-029-22	Sequence 22, App
106	19	1.0	4088	17	US-09-814-353-20949	Sequence 20949, A
107	19	1.0	4408	17	US-10-373-650-10	Sequence 10, App
108	19	1.0	6056	15	US-10-311-455-1000	Sequence 1000, App
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111	19	1.0	9759	15	US-10-373-650-1	Sequence 1, App
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113	19	1.0	45606	17	US-10-087-192-337	Sequence 337, App
114	19	1.0	47613	13	US-10-322-281-329	Sequence 329, App
115	19	1.0	59458	18	US-10-443-735-3	Sequence 3, App
116	19	1.0	63588	14	US-10-730-010-3	Sequence 3, App
117	19	1.0	63588	18	US-10-087-192-1966	Sequence 1966, App
118	19	1.0	72705	13	US-10-085-117-97	Sequence 97, App
119	19	1.0	86076	17	US-10-240-425-1470	Sequence 1470, App
120	19	1.0	120581	17	US-10-027-632-115	Sequence 115, App
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123	19	1.0	1223197	17	US-09-795-686-1	Sequence 1, App
124	19	1.0	1503841	9	US-09-946-807-1	Sequence 1, App
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127	19	1.0	1503841	9	US-09-933-797-582	Sequence 582, App
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134	19	1.0	1503841	9	US-09-736-457-1624	Sequence 1624, App
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136	19	1.0	1503841	9	US-09-902-941-1641	Sequence 1641, App
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C 233	18	0.9	761	17	US-10-027-632-14676	Sequence 14676, A	C 306	18	0.9	1871	14	US-10-174-572-301	Sequence 301, Appl
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C 246	18	0.9	936	13	US-10-774-355A-1265	Sequence 1265, A	C 319	18	0.9	1871	14	US-10-176-985-301	Sequence 301, Appl
C 247	18	0.9	976	13	US-10-027-632-31702	Sequence 31702, A	C 320	18	0.9	1871	14	US-10-176-985-301	Sequence 301, Appl
C 248	18	0.9	976	17	US-10-027-632-31702	Sequence 31702, A	C 321	18	0.9	1871	14	US-10-184-698-301	Sequence 301, Appl
C 249	18	0.9	1000	9	US-09-880-107-3462	Sequence 3462, Ap	C 322	18	0.9	1871	14	US-10-176-991-301	Sequence 301, Appl
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C 251	18	0.9	1014	17	US-10-062-674-1481	Sequence 1481, Ap	C 324	18	0.9	1871	14	US-10-173-697-301	Sequence 301, Appl
C 252	18	0.9	1050	17	US-10-369-493-24463	Sequence 24463, A	C 325	18	0.9	1871	14	US-10-173-697-301	Sequence 301, Appl
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C 272	18	0.9	1637	13	US-10-027-632-262160	Sequence 262160, A	C 345	18	0.9	1871	14	US-10-180-544-301	Sequence 301, Appl
C 273	18	0.9	1637	17	US-10-027-632-262160	Sequence 262160, A	C 346	18	0.9	1871	14	US-10-180-555-301	Sequence 301, Appl
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C 303	18	0.9	1871	14	US-10-180-557-301	Sequence 301, Appl	C 376	18	0.9	1871	14	US-10-184-616-301	Sequence 301, Appl

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Db	1801	TTGGGTTTGGAGCAACAGTCCCAAGAGGGCCACGATGAGAGCTTGCGCTTCTTAAAGA	1860
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; Sequence 41, Application US/10262666
; Publication No. US20030180298A1
; GENERAL INFORMATION:
; APPLICANT: Nakayama, Eiichi
; APPLICANT: Ono, Toshiro
; APPLICANT: Oid, Lloyd J.
; APPLICANT: Hasegawa, Kosei
; APPLICANT: Matsushita, Hirokazu
; TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
; FILE REFERENCE: L00461, 70140
; CURRENT APPLICATION NUMBER: US-10/262, 666
; PRIORITY FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/12497

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: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: US 60/356,937
: PRIOR FILING DATE: 2002-02-14
: PRIOR APPLICATION NUMBER: US 60/285,343
: PRIOR FILING DATE: 2001-04-20
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 41
: LENGTH: 1886
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (49)..(1680)
: OTHER INFORMATION:
US-10-262-666-41

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Query Match      99.5%; Score 1886; DB 16; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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OY	1	GTGAGAGCGGCTTGTGTCTCAGCGGAGCCGGGCGATCTTTCTCCGGCCATGTAGGAAGCCA	60
Db	1	GTTAGAGGCGGCTTGTGTCTCAGCGGAGCCGGGCGATCTTTCTCCGGCCATGTAGGAAGCCA	60
OY			
OY	61	GCCGCTGGCTTCTTCCCTCACTCTCTGAAGGTGCTCTCTGCACTCTGCGCA	120
Db	61	GCCGCTGGCTTCTTCCCTCACTCTCTGAAGGTGCTCTCTGCACTCTGCGCA	120
OY	121	GCCCAAGATTGACTCAGAGCCCTCCACTCAGGACGCTCTCTCTTACCGAATACGA	180
Db	121	GCCCAAGATTGACTCAGAGCCCTCCACTCAGGACGCTCTCTCTTACCGAATACGA	180
OY	181	CGTTCTTTCGACTGTGACTCTCAACTCGAAGGAGAGACTACGCGCGCTGCGTGA	240
Db	181	CGTTCTTTCGACTGTGACTCTCAACTCGAAGGAGAGACTACGCGCGCTGCGTGA	240
OY	241	ACCACAGGCTCCGGGAATCCCACTCGTCCAGCTGAGCAATATGAAAAACAAGGCTTA	300
Db	241	ACCACAGGCTCCGGGAATCCCACTCGTCCAGCTGAGCAATATGAAAAACAAGGCTTA	300
OY	301	GTGCCCGATGCTGTCTGTCTCCAACTCCCTTATGCTCTGCTGTTGATGTTCTGTG	360
Db	301	GTGCCCGATGCTGTCTGTCTCCAACTCCCTTATGCTCTGCTGTTGATGTTCTGTG	360
OY	361	CAGTTCACTCACTACCGTTGTCTCCACAACGCTCTACTATGCCAAGAAGTCCGTGTGCC	420
Db	361	CAGTTCACTCACTACCGTTGTCTCCACAACGCTCTACTATGCCAAGAAGTCCGTGTGCC	420
OY	421	CAGCAGTCTCTAATCTCTCACTCTAACACTCTCAAGAGAGATGAAAGCTTCACTGAAATC	480
Db	421	CAGCAGTCTCTAATCTCTCACTCTAACACTCTCAAGAGAGATGAAAGCTTCACTGAAATC	480
OY	481	TCACCCACACAGATGACTCTCCCCACTTCACCCCACTTCAAGTGAACAAGCCGACACC	540
Db	481	TCACCCACACAGATGACTCTCCCCACTTCACCCCACTTCAAGTGAACAAGCCGACACC	540
OY	541	TTTCCAGCTTGGCTGTGAGAGGCTCAGCAACAACGTGGAAGAGCTCTTCAATCTCTCTTG	600
Db	541	TTTCCAGCTTGGCTGTGAGAGGCTCAGCAACAACGTGGAAGAGCTCTTCAATCTCTCTTG	600
OY	601	TTCCTGGGAGGCGCAGAGACAGCGCBAAGCAACAGCAGAGACAGAGAGTGAAGCA	660
Db	601	TTCCTGGGAGGCGCAGAGACAGCGCBAAGCAACAGCAGAGACAGAGAGTGAAGCA	660
OY	661	CAGAGCCGACACAAGAAACAAGCAGGAAGGCGGCAAAACAAGAAAGCAAGAGAG	720
Db	661	CAGAGCCGACACAAGAAACAAGCAGGAAGGCGGCAAAACAAGAAAGCAAGAGAG	720
OY	721	GAAACAGAAAGAGAGGAAAGCAGAAAGAAAGCAAGGAGCTTAAAGAGGATCGGAGGCT	780
Db	721	GAAACAGAAAGAGAGGAAAGCAGAAAGAAAGCAAGGAGCTTAAAGAGGATCGGAGGCT	780

QY 781 GTGTCTGAGCTGAGACAGACTGACAGCCCAAGTTTCACTGAACTGATCTTTTAAAC 840
DB 781 GTGTCTGAGCTGAGACAGACTGACAGCCCAAGTTTCACTGAACTGATCTTTTAAAC 840
QY 841 CCTTCTCTTTTGTCTCTCCCGGGTACGAGAACTAGACTCTCTTAATGATGAGAAC 900
DB 841 CCTTCTCTTTTGTCTCTCCCGGGTACGAGAACTAGACTCTCTTAATGATGAGAAC 900
QY 901 ATCCAGAGAGCTCATTCAGTACAGCCAGAAATGATGAAATGAAATGAAATGAAATGAG 960
DB 901 ATCCAGAGAGCTCATTCAGTACAGCCAGAAATGATGAAATGAAATGAAATGAAATGAG 960
QY 961 AACTCTCTGAGAAACCAAAACCTTGAGCTTCTGACCTGACCTGACCTGACCTGACCT 1020
DB 961 AACTCTCTGAGAAACCAAAACCTTGAGCTTCTGACCTGACCTGACCTGACCTGACCT 1020
QY 1021 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 GCTTGAAGTACATGAGAGAGAGAGATCTTGGTTTGGGAAAGTGGTCTGAGACCTTT 1140
DB 1081 GCTTGAAGTACATGAGAGAGAGAGATCTTGGTTTGGGAAAGTGGTCTGAGACCTTT 1140
QY 1141 GGGCGGCGACATGATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 GGGCGGCGACATGATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TGGCACTGAG 1260
DB 1201 TGGCACTGAG 1260
QY 1261 GTGAGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 GTGAGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TCAAGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TCAAGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 CGGCTTGGCAAG 1440
DB 1381 CGGCTTGGCAAG 1440
QY 1441 CTTAGCTTCAAG 1500
DB 1441 CTTAGCTTCAAG 1500
QY 1501 CCAAACTAGCTTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 CCAAACTAGCTTCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TCCCGCATGAG 1620
DB 1561 TCCCGCATGAG 1620
QY 1621 GAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 GAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 GCTGAGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
DB 1681 GCTGAGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
QY 1741 ACCCAATGCTTCAAG 1800
DB 1741 ACCCAATGCTTCAAG 1800
QY 1801 TTGGGTTGAG 1860
DB 1801 TTGGGTTGAG 1860
QY 1861 TGACTTTACATTAATGTTATCTTC 1886

DB 1861 TGACTTTACATTAATGTTATCTTC 1886

RESULT 3
US-10-085-117-53
/ Sequence 53, Application US/10085117
/ Publication No. US2003023234A1
/ GENERAL INFORMATION:
/ APPLICANT: Morris, David W.
/ APPLICANT: Engelhard, Eric K.
/ TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
/ FILE REFERENCE: 529452000121
/ CURRENT APPLICATION NUMBER: US/10/085.117
/ PRIOR FILING DATE: 2002-02-27
/ NUMBER OF SEQ ID NOS: 361
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 53
/ LENGTH: 1886
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-085-117-53

Query Match 99.5%; Score 1886; DB 17; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGAAGCGGCTTGTGTCACAGGAGACGGGCGGATTTTTCGGCCATGAGAAAGCA 60
DB 1 GTTGAAGCGGCTTGTGTCACAGGAGACGGGCGGATTTTTCGGCCATGAGAAAGCA 60
QY 61 GCGCTGAGCTTCTTCCCTCCATCTCTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 GCGCTGAGCTTCTTCCCTCCATCTCTGAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 GCCAGAGATGACATCAGAGCCCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 GCCAGAGATGACATCAGAGCCCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GCGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GCGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ACCAAGCGCTGCGGAATCCCACTGCTCAGCTGAGACCAATGAAACACAGGCTTA 300
DB 241 ACCAAGCGCTGCGGAATCCCACTGCTCAGCTGAGACCAATGAAACACAGGCTTA 300
QY 301 GTGCGGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GTGCGGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 CAGTTCACTCAACCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CAGTTCACTCAACCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 CAGCGAGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 CAGCGAGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TACCCACAGATGAGACTGCGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 TACCCACAGATGAGACTGCGCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 TTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 TTCCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY	661	CAGAGCGCGACACAAGAACACAAGAGAAAGGGGCGAGAAACAGAAAGACGAAAGAG	720
Db	661	CAGAGCGCGACACAAGAACACAAGAGAAAGGGGCGAGAAACAGAAAGACGAAAGAG	720
QY	721	GAAACAGAAAGAGAGGAGAAACAGAGAAAGAGACAGAGGACTTAAAGAGGAGACGGAGGCT	780
Db	721	GAAACAGAAAGAGAGGAGAAACAGAGAAAGAGAGAGAGACAGGAGACTTAAAGAGGAGACGGAGGCT	780
QY	781	GTGTCTCAGCTGCGACAGACTCAGAGCCCAAATTTCACCTGAAATCTCTATCTTCTAAC	840
Db	781	GTGTCTCAGCTGCGACAGACTCAGAGCCCAAATTTCACCTGAAATCTCTATCTTCTAAC	840
QY	841	CCCTTCCTCTTTTGGCTCCCCGGGGTACGAAAGTAGAGTCTACCTCTATGATATAGAGAAC	900
Db	841	CCCTTCCTCTTTTGGCTCCCCGGGGTACGAAAGTAGAGTCTACCTCTATGATATAGAGAAC	900
QY	901	ATCCAGAGAGCTCATTCGATTCAGCCCGAGGAAATAGATGAAATGAAATGAAATATATAGTAG	960
Db	901	ATCCAGAGAGCTCATTCGATTCAGCCCGAGGAAATAGATGAAATGAAATGAAATATATAGTAG	960
QY	961	AACCTCTA CTGAGAAACCAAAACCCTGGCAGCTTCTG CAGCTGCCCA CACAGAGCC	1020
Db	961	AACCTCTA CTGAGAAACCAAAACCCTGGCAGCTTCTG CAGCTGCCCA CACAGAGCC	1020
QY	1021	TTTGCTGAGCTGTGTGTTTCGATCGTGAAGTAATCTGCACTCATATACCCCA CAGCCAAAG	1080
Db	1021	TTTGCTGAGCTGTGTGTTTCGATCGTGAAGTAATCTGCACTCATATACCCCA CAGCCAAAG	1080
QY	1081	GCCTGGAAGTACATGAGAGAGAGAGATCCTTGSGTTCCGGGAAAGTGGGTCTGAGACGCTT	1140
Db	1081	GCCTGGAAGTACATGAGAGAGAGAGATCCTTGSGTTCCGGGAAAGTGGGTCTGAGACGCTT	1140
QY	1141	GGGCGGCGACACATGTCTTACCTGTGACCCTGTGTGACTTCTGCTCCTTGGAACCTGGAGCAG	1200
Db	1141	GGGCGGCGACACATGTCTTACCTGTGACCCTGTGTGACTTCTGCTCCTTGGAACCTGGAGCAG	1200
QY	1201	TGCGCATTCAGAGGCGCAGCTCGAGGGGCAACATATGCGACACCTCCCA CAGACTCCCTTT	1260
Db	1201	TGCGCATTCAGAGGCGCAGCTCGAGGGGCAACATATGCGACACCTCCCA CAGACTCCCTTT	1260
QY	1261	GTCAAGCCCTTGCTTGCTGCCAGAGCCGTGCCATCCGCAACAGAGTAGGGTCCCCAGAA	1320
Db	1261	GTCAAGCCCTTGCTTGCTGCCAGAGCCGTGCCATCCGCAACAGAGTAGGGTCCCCAGAA	1320
QY	1321	TCAGGCGGCTTTTACGGGCTGATTTTGAACGGTGGGCTCCCATATGAGCTTCTGGTGTGCC	1380
Db	1321	TCAGGCGGCTTTTACGGGCTGATTTTGAACGGTGGGCTCCCATATGAGCTTCTGGTGTGCC	1380
QY	1381	CGGCTTGGCCAGAAAGGCTGTGAAGATGTCCGAGTCTCTGGGTGGCTTCAGACTGAGTTTC	1440
Db	1381	CGGCTTGGCCAGAAAGGCTGTGAAGATGTCCGAGTCTCTGGGTGGCTTCAGACTGAGTTTC	1440
QY	1441	CTTAGCTTCCAGGATGGGGATTTTCCCTTACCAAGATTGTGTGACACGACTATATCCAGTAC	1500
Db	1441	CTTAGCTTCCAGGATGGGGATTTTCCCTTACCAAGATTGTGTGACACGACTATATCCAGTAC	1500
QY	1501	CCAAACTACTGTTCCTTCAAAAAGCAGCAGGTGCTGATGAGAAACCGCAATCCGAAAGGTTG	1560
Db	1501	CCAAACTACTGTTCCTTCAAAAAGCAGCAGGTGCTGATGAGAAACCGCAATCCGAAAGGTTG	1560
QY	1561	TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGGCGCTGAGGCCCTGGCAAAAGTAG	1620
Db	1561	TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTGGCGCTGAGGCCCTGGCAAAAGTAG	1620
QY	1621	GACGTTGTGCTTCGATGAGAGCCAGAGATTCAAGACTTGAAGCCAGATTCCGATGAGA	1680
Db	1621	GACGTTGTGCTTCGATGAGAGCCAGAGATTCAAGACTTGAAGCCAGATTCCGATGAGA	1680
QY	1681	GCTGAGCGCTATTTCTGCGCCACACCCGACCCAACTGCGCCAGCTTCTATATGTTTGTAG	1740
Db	1681	GCTGAGCGCTATTTCTGCGCCACACCCGACCCAACTGCGCCAGCTTCTATATGTTTGTAG	1740
QY	1741	ACCCCAATGTCTTACGAGCTGCCCTTCTGGGTCTGTATCTGGGCCCTTACTCACAATTTCC	1800

D _b	1741	ACCCCATTTGCTTTAGAGCTGCCCCCTTCTGGGTCGTGTACTGGGCCCTACTCAATTTCC	1800
O _Y	1801	TTGGGTTGAGCAACAGTCCCGAGAGAGGCGCAGGTGGAGCTGGCCCTCTTAAAGA	1860
D _b	1801	TTGGGTTGAGCAACAGTCCCGAGAGAGGCGCAGGTGGAGCTGGCCCTCTTAAAGA	1860
O _Y	1861	TGACTTACATAAATGTTGATCTTC	1886
D _b	1861	TGACTTACATAAATGTTGATCTTC	1886

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RESULT 4
US-10-085-117-54
: Sequence 54, Application US/10085117
: Publication No. US2003023234A1
: GENERAL INFORMATION:
: APPLICANT: Morris, David W
: TITLE OF INVENTION: NOVEL COMPOSITIONS AND
: FILE REFERENCE: 529452000121
: CURRENT APPLICATION NUMBER: US/10/085,117
: PENDING FILING DATE: 2002-02-27
: PRIOR APPLICATION NUMBER: US 09/798,586
: PRIOR FILING DATE: 2001-03-02
: NUMBER OF SEQ IDS NOS: 361
: SOFTWARE: PatsSQ for Windows Version 4.0
: SEQ ID NO 54
: LENGTH: 1632
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-085-117-54

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Query Match	86.1%;	Score 1632;	DB 17;	Length 1632;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1632;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy		49	ATGAGGAAGCAGACCGCTGGCTTCTTCCTCCATCACTCTGAAGATGTGTCTCGCTCTTG	108
Db		1	ATGAGGAAGCAGACCGCTGGCTTCTTCCTCCATCACTCTGAAGATGTGTCTCGCTCTTG	60
Oy		109	GCACCTGCGCAGGCCAGAGATTCCAGTCAAGCCCCCATCTCCAGGCAGCCCTCTCTCTCT	168
Db		61	GCACCTGCGCAGGCCAGAGATTCCAGTCAAGCCCCCATCTCCAGGCAGCCCTCTCTCTCT	120
Oy		169	ACCGAATAACAACGGTTCTTTCGACATGCTGACTCCACCCTGSAAGSAGAATACTATCTGC	228
Db		121	ACCGAATAACAACGGTTCTTTCGACATGCTGACTCCACCCTGSAAGSAGAATACTATCTGC	180
Oy		229	CGTCTCCGTGCAACCCACGAGCTGCCGGAATCCACACATCTGTCACTGGACCAATATGAA	288
Db		181	CGTCTCCGTGCAACCCACGAGCTGCCGGAATCCACACATCTGTCACTGGACCAATATGAA	240
Oy		289	AACCAAGGCTTAATGAGCCGAGTAGTGTCTGTCTCCAACCTCCCTATATGACCTCTGCTTT	348
Db		241	AACCAAGGCTTAATGAGCCGAGTAGTGTCTGTCTCCAACCTCCCTATATGACCTCTGCTTT	300
Oy		349	GAGTCTTCTTCGACAGTTCACTCACTACGGTTGCTCCAAACAAGTCTATATGACCAAGAA	408
Db		301	GAGTCTTCTTCGACAGTTCACTCACTACGGTTGCTCCAAACAAGTCTATATGACCAAGAA	360
Oy		409	GTCTGTGTTCCGACGACGCTCTAATTCTTCACCTTAACCTTAAGGAATTAAGAAGT	468
Db		361	GTCTGTGTTCCGACGACGCTCTAATTCTTCACCTTAACCTTAAGGAATTAAGAAGT	420
Oy		469	TCACTGAAGTCTCAACCCACCAAGATGACTTCCCCTATCTCACCCCACTTTCACAGTGA CA	528
Db		421	TCACTGAAGTCTCAACCCACCAAGATGACTTCCCCTATCTCACCCCACTTTCACAGTGA CA	480
Oy		529	GAAAGCCAGACTTCCAGGACCTGTGAGAGAGCTCAACAACAAGTGAABAAGCTCTTA	588
Db		481	GAAAGCCAGACTTCCAGGACCTGTGAGAGAGCTCAACAACAAGTGAABAAGCTCTTA	540

Db 125 GAACTCAGGCTCCAGCTCAGGAGCCCTCTCTCTCCATCCGAAATACGAGCCTTCTCG 184
Qy 191 CACTGCTGATCTCCAACTTGGAGGAGAGACTACCTGCGCTCTCCGTCGACACCCAGCCT 250
Db 185 CACTGCTGATCTCCAACTTGGAGGAGAGACTACCTGCGCTCTCCGTCGACACCCAGCCT 244
Qy 251 GCCGGAATCCCACTGCTCAGCTGGAACCAATATGAAAACCAAGGCTTACGCGCATG 310
Db 245 GCCGGAATCCCACTGCTCAGCTGGAACCAATATGAAAACCAAGGCTTACGCGCATG 304
Qy 311 GTGCTGCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
Db 305 GTGCTGCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
Qy 371 ACTACCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430
Db 365 ACTACCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Qy 431 CTATTCCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
Db 425 CTATTCCTGCTCCAACTTCCCTTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
Qy 491 CGATGCTCTCCCTCCATCTCACCCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 550
Db 485 CGATGCTCTCCCTCCATCTCACCCTTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 544
Qy 551 GGCTTGAAGGCTCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 610
Db 545 GGCTTGAAGGCTCAGAGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
Qy 611 GCCGAGGAG 670
Db 605 GCCGAGGAG 664
Qy 671 CACAAGAACACAG 730
Db 665 CACAAGAACACAG 724
Qy 731 AG 790
Db 725 AG 784
Qy 791 TGCAGACAGACTCAG 850
Db 785 TGCAGACAGACTCAG 844
Qy 851 TTGCTCTCCCGGCTCAG 910
Db 845 TTGCTCTCCCGGCTCAG 904
Qy 911 TCATTCGATCAG 970
Db 905 TCATTCGATCAG 964
Qy 971 GAG 1030
Db 965 GAG 1024
Qy 1031 TTGCTCTCCCGGCTCAG 1090
Db 1025 TTGCTCTCCCGGCTCAG 1084
Qy 1091 ACATGAG 1150
Db 1085 ACATGAG 1144
Qy 1151 ACATGCTCTACCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1210
Db 1145 ACATGCTCTACCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1204
Qy 1211 AGGCGAGCTGAG 1270
Db 1205 AGGCGAGCTGAG 1264

Qy 1271 TGCTTGCTCCAGAGAGCTCTCCATCGGAGACAGAGTAAAGGTATCCAGAGATAGAGCCGT 1330
Db 1265 TGCTTGCTCCAGAGAGCTCTCCATCGGAGAGACAGAGTAAAGGTATCCAGAGATAGAGCCGT 1324
Qy 1331 TTTCAGGCTGAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCTGCTGCT 1390
Db 1325 TTTCAGGCTGAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCTGCTGCT 1384
Qy 1391 CGAAAGGCTGAGAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCTGCTGCT 1450
Db 1385 CGAAAGGCTGAGAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCTGCTGCT 1444
Qy 1451 AGATGAGGATTTCCCTCAAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCT 1510
Db 1445 AGATGAGGATTTCCCTCAAGATTTGTAAGGTGGGCTCCACATGAGACTTCTGCTGCTGCT 1504
Qy 1511 GTTCCTTCAAAAGGAG 1570
Db 1505 GTTCCTTCAAAAGGAG 1564
Qy 1571 GATGCTGAGATGAGACTTACAGTGGCTGAGCC 1606
Db 1565 GATGCTGAGATGAGACTTACAGTGGCTGAGCC 1600

RESULT 7
US-09-397-945-90

/ Sequence 90, Application US/09397945
/ Publication No. US20030065139A1
/ GENERAL INFORMATION:

/ APPLICANT: Human Genome Sciences, Inc. et al.
/ TITLE OF INVENTION: 95 Human secreted proteins
/ FILE REFERENCE: P2027P1

/ CURRENT FILING DATE: 1999-09-17
/ CURRENT FILING DATE: 1999-09-17

/ PRIOR APPLICATION NUMBER: PCT/US99/05804
/ PRIOR FILING DATE: 1999-03-18

/ PRIOR APPLICATION NUMBER: 60/078,566
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,576
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,573
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,574
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,579
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/080,314
/ PRIOR FILING DATE: 1998-04-01

/ PRIOR APPLICATION NUMBER: 60/080,312
/ PRIOR FILING DATE: 1998-04-01

/ PRIOR APPLICATION NUMBER: 60/078,578
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,581
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,577
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/078,563
/ PRIOR FILING DATE: 1998-03-19

/ PRIOR APPLICATION NUMBER: 60/080,313
/ PRIOR FILING DATE: 1998-04-01

/ NUMBER OF SEQ ID NOS: 470
/ SOFTWARE: Patent In Ver. 2.0

/ SEQ ID NO 90
/ LENGTH: 1892

/ TYPE: DNA
/ ORGANISM: Homo sapiens

/ US-09-397-945-90

Query Match

Best Local Similarity 67.8%; Score 1284; DB 10; Length 1892;
Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;


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? PRIOR APPLICATION NUMBER: 60/080,314
? PRIOR FILING DATE: 1998-04-01
? PRIOR APPLICATION NUMBER: 60/080,312
? PRIOR FILING DATE: 1998-04-01
? PRIOR APPLICATION NUMBER: 60/078,578
? PRIOR FILING DATE: 1998-03-19
? Remaining Prior Application data removed - See File Wrapper or PAM
? NUMBER OF SEQ ID NOS: 470
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 90
? LENGTH: 1892
? TYPE: DNA
? ORGANISM: Homo sapiens
?
US-10-653-595-90

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Query Match	67.8%	Score 1284;	DB 17;	Length 1892;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1794;				

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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Db	802	GTTCACCTGAACTCTATCTTTCAACCTTCCCTTTTGTCTCCCGGGTACGAAAGT	861
OY	873	AGAGCTACACTCTATATGTAATGGAGAAACATCCAGAGCTCATTTGATCAGCCCCAGGAAAT	932
Db	862	AGAGCTACCTCTATATGTAATGGAGAAACATCCAGAGCTCATTTGATCAGCCCCAGGAAAT	921
OY	933	AGATGAAATGAATGAAATATATATGATGAGAACTCTTACCTGAGAAACCAAAACCTTCGCAG	992
Db	922	AGATGAAATGAATGAAATATATATGATGAGAACTCTTACCTGAGAAACCAAAACCTTCGCAG	981
OY	993	CTTCCTGCAGCTGCCCCACACAGAGGGCTTGTGTGTGTGTGTATTTGATGTGAGAA	1052
Db	982	CTTCCTGCAGCTGCCCCACACAGAGGGCTTGTGTGTGTGTGTATTTGATGTGAGAA	1040
OY	1053	TATCTGCATCATTAACCCCAACAGCCAGAGGCTGTGAAATGATCAGGAGAGAGATCTTTGG	1112
Db	1041	TATCTGCATCATTAACCCCAACAGAGGCTGTGAAATGATCAGGAGAGAGATCTTTGG	1100
OY	1113	TTTCGGGAAAGTCGGATCTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCCCTGTG	1172
Db	1101	TTTCGGGAAAGTCGGATCTGTGACAGCCTTGGGCGGCGACACATGTCTACCTGTGCCCTGTG	1160
OY	1173	TGACTTCTGTCTCTTTGAAAGCTGAGCAGTCCACTCAGAGCCAGCCTGACGGCGAAC	1232
Db	1161	TGACTTCTGTCTCTTTGAAAGCTGAGCAGTCCACTCAGAGCCAGCCTGACGGCGAAC	1220
OY	1233	ATTCGACACCTCCCAACAAAGCTCCCTTTGTGACGCCCCCTTGTCTTCACAGAGCCTGTTC	1292
Db	1221	ATTCGACACCTCCCAACAAAGCTCCCTTTGTGACGCCCCCTTGTCTTCACAGAGCCTGTTC	1279
OY	1293	CATTCGGCAACGAGTATGGATCCCAAGATCAGAGCGGCTTTTACGGGCTGGAATTTTGAACG	1352
Db	1280	CATTCGGCAACGAGTATGGATCCCAAGATCAGAGCGGCTTTTACGGGCTGGAATTTTGAACG	1339
OY	1353	TGGGCTCCACATGGACTTCTGTGTGTGCCCGCTTTGCCACGAAAGGCTGTGAAGATGTCCG	1412
Db	1340	TGGGCTCCACATGGACTTCTGTGTGTGCCCGCTTTGCCACGAAAGGCTGTGAAGATGTCCG	1399
OY	1413	AGTCTCTGGGTGGCTCCAGACTGAGTTCTTACCTTCCAGATGGAGATTTCCCTACCA	1472
Db	1400	AGTCTCTGGGTGGCTCCAGACTGAGTTCTTACCTTCCAGATGGAGATTTCCCTACCA	1458
OY	1473	GATTTGTGACACAGATATATCCAGTACCCAACTATCTTTCTTCAAAAGCGAGCATGTG	1532
Db	1459	GATTTGTGACACAGATATATCCAGTACCCAACTATCTTTCTTCAAAAGCGAGCATGTG	1518
OY	1533	TCTGATGAAACCGCAATCGAAGGATCCCGCATGAGATGTCTGCGAATGAGACTTGA	1592
Db	1519	TCTGATGAAACCGCAATCGAAGGATCCCGCATGAGATGTCTGCGAATGAGACTTGA	1578
OY	1593	CAGTGCCTGAGCCCTTGGCAAAAGTAGAGCGTTGTGATGAGAGCCAGGAGTTTCCG	1652
Db	1579	CAGTGCCTGAGCCCTTGGCAAAAGTAGAGCGTTGTGATGAGAGCCAGGAGTTTCCG	1638
OY	1633	CACCTTGACCTTATGAGCAGTTCGAGTATGAGCTGTGGCTATTTCTGCCACACCCACGCCA	1712
Db	1619	CACCTTGACCTTATGAGCAGTTCGAGTATGAGCTGTGGCTATTTCTGCCACACCCACGCCA	1698
OY	1713	ACCTGCGCACGTTCTATTTGTTTGAACCCCAATGCTTTTGAAGGCGCCCTTCTGGGT	1772
Db	1699	ACCTGCGCACGTTCTATTTGTTTGAACCCCAATGCTTTTGAAGGCGCCCTTCTGGGT	1758
OY	1773	CTGTATCTAGGCGCCCTACACATTTCTTGGGTGAGCAACAGTCCACAGAGAGGCGCA	1832
Db	1759	CTGTATCTAGGCGCCCTACACATTTCTTGGGTGAGCAACAGTCCACAGAGAGGCGCA	1818

RESULT 9
US-10-296-115-693
; Sequence 693, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc


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? LENGTH: 964
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 21..527
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 21..95
? OTHER INFORMATION: Von Heijne matrix
? OTHER INFORMATION: score 8.5
? FEATURE:
? NAME/KEY: polyA_signal
? LOCATION: 921..926
? FEATURE:
? NAME/KEY: polyA_site
? LOCATION: 953..963
?
US-09-578-360A-262

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Query Match	27.9%	Score 528;	DB 11;	Length 964;
Best Local Similarity	99.3%;			
Matches 948; Conservative		Pred. No. 6.4e-268;		

[illegible]

Db 722 AAGGACAGGGGACTTAAGGAGGACGGGAGGCTGTGCTACGTGAGACAGACTTAGAGC 78
Qy 809 CCAAGTTTCACCTGGAATCTCTATCTCTTAAACCTCCCTCTTTTCTGCCCGGAGTACGAG 86
Db 782 CCAATTTCACCTGATCTGATCTCTATCTTTTAACTCTCTCTTTTCTCCCGGATACGAG 84
Qy 869 AAGTAGACTCTACCTCCATATATATGAGAACATCCAGAGCTCATTCGATCAGCCCAAG 92
Db 842 AAGTAGACTCTACCTCATGATATAGGAGAACATCCAGACTCATTCGATCAGCCCAAG 92
Qy 929 AATATGATGAATGAATGAATGAATATATATGATGAGAACTCCTTACTGAGAGAACCAAAA 98
Db 902 AATATGATGAATGAATGAATATATATGATGAGAACTCCTTACTGAGAGAACCAAAA 95

RESULT 11
US-10-719

; Sequence 6794, Application US/10719993
 ; Publication No. US20040265849A1
 ; GENERAL INFORMATION:
 ; Application No. 10/719,993

```

1  ORGANISM: CARGILL, Michele et al.
2  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
3  TITLE OF INVENTION: ALZHEIMER'S DISEASE. METHODS OF
4  FILE REFERENCE: CL001496
5  CURRENT APPLICATION NUMBER: US/10/719,993
6  CURRENT FILING DATE: 2003-11-24
7  NUMBER OF SEQ ID NOS: 55342
8  SOFTWARE: FastSeq For Windows Version 4.0
9  SEQ ID NO: 6794
10 LENGTH: 21347
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 US-10-719-993-6794

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00-10-119-993-6794

Query Match	24.9%	Score 471	DB 18	Length 21347
Best Local Similarity	100.0%	Pred. No. 7.1e-238		
Matches 471; Conservation				

[illegible]

US-10-085-117-52
 ; Sequence 52, Application US/10085117
 ; Publication No. US2003023234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 529452000121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52
 ; LENGTH: 29346
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variation
 ; LOCATION: (1)...(29346)
 ; OTHER INFORMATION: n = any nucleotide
 US-10-085-117-52

Query Match 24.9%; Score 471; DB 17; Length 29346;
 Best Local Similarity 100.0%; Pred. No. 7e-238;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 AGTGAAGAAAGCCGACACCTTCCAGCCCTTGAGAGGCTCAGCAACAGCTGGAGA 561
 DB 12812 AGTGAAGAAAGCCGACACCTTCCAGCCCTTGAGAGGCTCAGCAACAGCTGGAGA 12871
 QY 582 GCTCCACAAATCCTCTGCTGCTGAGAGGCGCAGAGCAAGCCGAGCAAGCAAGCAAGCA 641
 DB 12872 GCTCCACAAATCCTCTGCTGCTGAGAGGCGCAGAGCAAGCCGAGCAAGCAAGCAAGCA 12931
 QY 642 GCAGAGAGTGAGACAGGAGGAGGCGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 701
 DB 12932 GCAGAGAGTGAGACAGGAGGAGGCGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 12991
 QY 702 ACAGAGAGAGCAAGAGAGAGCAAG 761
 DB 12992 ACAGAGAGAGCAAGAGAGAGCAAG 13051
 QY 762 TAAG 821
 DB 13052 TAAG 13111
 QY 822 TGAATCTATCTTCTTAACCTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 881
 DB 13112 TGAATCTATCTTCTTAACCT 13171
 QY 882 TCTATGATATGAG 941
 DB 13172 TCTATGATATGAG 13231
 QY 942 GATGAAATATATGAG 992
 DB 13232 GATGAAATATATGAG 13282

RESULT 13
 US-09-918-995-14842
 ; Sequence 14842, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HySeq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14842
 ; LENGTH: 469
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(469)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-14842

Query Match 20.0%; Score 379; DB 10; Length 469;
 Best Local Similarity 99.8%; Pred. No. 3.6e-189;
 Matches 429; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 936 TGAATGAATGAATATATGATGAG 995
 DB 40 TGAATGAATGAATATATGATGAG 99
 QY 996 CCTGAG 1055
 DB 100 CCTGAG 159
 QY 1056 CTGCATCATTAACCCCAAG 1115
 DB 160 CTGCATCATTAACCCCAAG 219
 QY 1116 CGGAG 1175
 DB 220 CGGAG 279
 QY 1176 CTTCGCTCTCTTGAAG 1235
 DB 280 CTTCGCTCTCTTGAAG 339
 QY 1236 CGAG 1295
 DB 340 CGAG 399
 QY 1296 CGGAG 1355
 DB 400 CGGAG 459
 QY 1356 GCTCCACATG 1365
 DB 460 GCTCCACATG 469

RESULT 14
 US-10-719-993-7043
 ; Sequence 7043, Application US/10719993
 ; Publication No. US20040265849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001496
 ; CURRENT APPLICATION NUMBER: US/10/719,993
 ; CURRENT FILING DATE: 2003-11-24
 ; NUMBER OF SEQ ID NOS: 55342
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7043
 ; LENGTH: 24923
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(24923)
 ; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;

Query Match 17.3%; Score 328; DB 18; Length 24923;
Best Local Similarity 100.0%; Pred. No. 2.6e-162;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 522 AGTGCAGAGAGCCAGACCTTCCAGCCCTGAGAGGCTCAGAGAAAGCTGAGAA 581
DB 24596 AGTGCAGAGAGCCAGACCTTCCAGCCCTGAGAGGCTCAGAGAAAGCTGAGAA 581
QY 582 GCTCTCAATCTCTCTTGTCTTGTCTGAGAGGCGAGAGCGCAAGCGCAAGCAAGCA 24655
DB 24656 GCTCTCAATCTCTCTTGTCTTGTCTGAGAGGCGAGAGCGCAAGCGCAAGCAAGCA 24655
QY 642 GCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24715
DB 24716 GCAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24715
QY 702 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24775
DB 24776 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24775
QY 762 TAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24835
DB 24836 TAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24835
QY 822 TGAATCTCTATCTTCTTAACCTTCTCT 849
DB 24896 TGAATCTCTATCTTCTTAACCTTCTCT 24923
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RESULT 15

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US-09-918-995-36471
/ Sequence 36471, Application US/09918995
/ Publication No. US20030073623A1
/ GENERAL INFORMATION:
/ APPLICANT: Hwaseq, Inc.
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
/ TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
/ FILE REFERENCE: 20411-756
/ CURRENT APPLICATION NUMBER: US/09/918, 995
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235, 076
/ NUMBER OF SEQ ID NOS: 1999-01-20
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 36471
/ LENGTH: 474
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(474)
/ OTHER INFORMATION: n = A,T,C or G
US-09-918-995-36471
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Query Match 16.2%; Score 307; DB 10; Length 474;
Best Local Similarity 99.5%; Pred. No. 4e-151;
Matches 407; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 696 GCAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755
DB 66 GCAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755
QY 756 GGGGACTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
DB 126 GGGGACTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 125
QY 816 TCACTCTGAATCTCTATCTTCTTAACCTTCTCTTGTCTCCCGGTTAGAGAGATGA 185
DB 186 TCACTCTGAATCTCTATCTTCTTAACCTTCTCTTGTCTCCCGGTTAGAGAGATGA 185
QY 876 GTCTACTCTATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
DB 246 GTCTACTCTATGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
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QY 936 TGAATGAATGAATATATATATATATATATATATATATATATATATATATATAT 995
DB 306 TGAATGAATGAATATATATATATATATATATATATATATATATATATATATAT 995
QY 996 CTGCAAGCTGCCCCACACAGAGGCTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1055
DB 366 CTGCAAGCTGCCCCACACAGAGGCTTGTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1055
QY 1056 CTGCATCATTAACCCCAAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1104
DB 426 CTGCATCATTAACCCCAAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
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Search completed: March 8, 2005, 06:25:49
Job time : 2091 secs

us-09-559-013e-23.rtf

TITLE OF INVENTION: Schellenger, Gerald D.
 NUMBER OF SEQUENCES: 209
 CORRESPONDENCE ADDRESSES: WERNER'S SYNDROME
 ADDRESSEE: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6500
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/618,166
 FILING DATE: 17-Jul-2000
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: McMaisters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 240052.419C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682-6200
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16442 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 208:
 US-09-618-166-208

[illegible]

RESULT 7
 US-09-949-016-16775/c
 Sequence 16775, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498

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/ PRIOR FITTING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0.
/ SEQ ID NO 16775
/ LENGTH: 12695
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16775

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	Query Match	3.8%	Score 72.2	DB 4	Length 12695
	Best Local Similarity	55.9%	Pred. No. 1.4e-09		
	Matches 137	Conservative 0	Mismatches 108	Indels 0	Gaps 0
QY	563	TCAGCAACACGTGGAGAGCTCTTCAATCTCTTGTCTCTGGAGGCCAGAGACAAAG	622		
Db	9739	TCAGTGAAGCAGGSCCAGAGACATCTCACTAGCTGAGAGAGCAAGAGAGAGAGAG			
QY	623	CGCCAGAGCACAAGCAGAGCCAAAGATGTGAGCAACAGCCAGAGCCGACAAAGAACCA	682		
Db	9679	AGAGAGAGGAAG	682		
QY	603	AGCAGAAAGGGGCGAGAAACAGAAAGCACAAGAAAGGAAACAGAAAGAGAGGGAAAGC	9620		
Db	9619	AGGAG	742		
QY	743	AGGAAAGAGACAGGGGACTTAAAGAGGACGGAGAGCTGTCTCAGCTGGAGCAACT	802		
Db	9559	AGGAAAG	802		
QY	803	CAGAG 807			
Db	9499	AGGAG 9495			

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RESULT 8
US-09-249-585A-2
/ Sequence 2, Application US/09249585A
/ Patent No. 6417002
/ GENERAL INFORMATION:
/ APPLICANT: HORIICK, Robert
/ TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
/ FILE REFERENCE: 0867/00905
/ CURRENT APPLICATION NUMBER: US/09/249,585A
/ PRIORITY FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 2
/ LENGTH: 1926
/ TYPE: DNA
/ ORGANISM: Epstein Barr Virus
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1926)
/ OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

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Query Match	3.88!	Score 71.2;	DB 3;	Length 1926;
Best Local Similarity	61.2%;	Pred. No. 9.2e-10;		
Matches 115;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0
QY	613	CAGAGCAACCGCCACAGACACAAACAGAGGCAAGAGTGTGAGCACAGGACGAGCCGACACA	672	
Db	377	CAGAGAGAGCGGCGACAGAGGACAGAGGAGCGGGCAGAGAGGGGACAGAGGGGCGACAGAGCAGAGG		
QY	673	CAGAAACAACCCAGAGAAAGAGGGGACAGAAACAGAAAGATCAGACAGAGAAACAGGAAGAG	436	
Db	437	GAGGGGCAAGAACACAGAGAGAGGGGCAAGAGGGCCAGAGACACAGAGAGAGGCGCAGAGAGGGG	732	
QY	733	GAGGGAACACAGAAAGAAAGGACAGAGGGACTTAAAGAGGAGCGGGAAGCTGTCTTCACGCTG	496	
Db	497	CAGAGGGGCAAGAGACAGAGAGAGGGGACAGAGACAGAGAGAGAGGGGCAAGAGAGGGCCAGAGG	792	
QY	793	CAGACAGA 800		556

US-08-910-647-1
Sequence 1, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 08:22:56 ; Search time 1053 Seconds
(without alignments)
10653.286 Million cell updates/sec

Title: US-09-559-013E-23
Perfect score: 1895
Sequence: 1 gttgagcgcgtctgtctc.....tggtgactctcaaaaaaaaa 1895

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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13: geneseqn2004bs:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1895	100.0	1895	5	AAD08658 Human can
2	1890.2	99.7	1912	3	AAZ50927 Human pro
3	1886	99.5	1886	8	ABT14679 Human can
4	1856.4	98.0	1899	2	AAZ06785 Human adu
5	1811.2	95.6	1892	2	AAZ24890 Human sec
6	1811.2	95.6	1892	8	ADA39940 Human sec
7	1811.2	95.6	1892	10	ADC73578 Human sec
8	1811.2	95.6	1892	10	ADD37623 Human sec
9	1811.2	95.6	1892	10	ADA56130 Gene enco
10	1476.6	77.9	1854	9	ADA45034 Human pol
11	1271.8	67.1	1671	4	AAH98858 Human pro
12	992.8	52.4	3306	12	AD024565 Human pro
13	937.6	49.4	964	12	ADP19006 Human sec
14	937.6	49.4	964	2	AAZ97739 Novel can
15	479.2	25.3	695	13	ADQ53839 Human adu
16	433.8	22.9	469	9	ACH27630 Human leu
17	408.4	21.6	474	9	ACH49259 Human ful
18	339	17.9	516	8	ABZ72003 Human can
19	337.2	17.8	522	8	ABZ71705 Human can
20	329.8	17.4	507	8	ABZ71923 Human can

21	282.4	14.9	308	2	AAV88163 EST clone
22	199	10.5	199	8	ABZ19225 Group III
23	126.6	6.7	370	6	ABZ569017 Novel mur
24	124.4	6.6	128	2	AAZ51481 Human sec
25	81.2	4.3	30191	12	ADQ97654 Mouse can
26	75.6	4.0	28796	11	ACN44712 Mouse gen
27	74	3.9	628	12	ACH89664 Human gen
28	73.4	3.9	51259	2	AAZ83007 Partial m
29	72.6	3.8	16442	2	AAZ83006 Nucleotid
30	71.2	3.8	799	2	AAV55831 Nucleotid
31	71.2	3.8	1925	2	AAZ09924 Epstein B
32	71.2	3.8	1926	3	AAZ05254 Epstein B
33	71.2	3.8	1926	4	AAZ82902 EBV teche
34	71.2	3.8	1926	10	ADR65580 Human her
35	71.2	3.8	2580	3	AAZ75454 Nucleotid
36	71.2	3.8	2580	6	AAZ64275 Nucleotid
37	71.2	3.8	5452	2	AAZ09923 Anti-sens
38	71.2	3.8	8705	2	AAZ23778 Vector ps
39	71.2	3.8	8705	12	ADM10659 Expressio
40	71.2	3.8	9482	12	ADP64415 Vector pc
41	71.2	3.8	9600	2	AAV21683 Vector pl
42	71.2	3.8	10285	6	ABZ71027 PCBP-Xa-F
43	71.2	3.8	10285	6	ABZ66453 Plasmid p
44	71.2	3.8	10330	12	ADL67154 Plasmid p
45	71.2	3.8	10380	2	AAZ22248 Nucleotid

ALIGNMENTS

RESULT 1

ID AAD08658 standard; cDNA; 1895 BP.

XX AAD08658; (first entry)

DT 04-SEP-2001

DE Human cancer associated antigen OY-TES-1 cDNA.

XX Human, OY-TES-1; cytosolic; gene therapy; vaccine; fibrosarcoma cancer;

KW human associated antigen; ss.

XX Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS /tag= a /product= "Human OY-TES-1 protein"

FT primer_bind /bound_moiety= "Tes-N1 primer"

FT primer_bind /tag= c /complement (749..768)

FT primer_bind /bound_moiety= "ht-5 (sense) primer"

FT primer_bind /tag= d /bound_moiety= "GSP2-T1 primer"

FT primer_bind /tag= e /bound_moiety= "GSP1-T1 primer"

FT primer_bind /tag= f /bound_moiety= "ht-3 (anti-sense) primer"

FT primer_bind /tag= g /bound_moiety= "ht-5 (anti-sense) primer"

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XX 01-DEC-2000; 2000WO-US032750.
 PF 01-DEC-1999; 99US-016833P.
 PR 26-APR-2000; 2000US-00559013.
 XX
 PA (LUDWIG INST CANCER RES.
 PI Ono T, Nakayama E;
 XX WPI; 2001-397941/42.
 DR P-PSDB; AAE04382.
 XX
 PT Isolated polypeptide, useful in treating disorders such as cancer, is
 XX encoded by a nucleic acid (NA) Group 3 or 4 molecule.
 PS Claim 56; Fig 2; 127pp; English.
 CC The invention relates to cancer associated antigens and their nucleic
 CC acids which are expressed in methylcholanthrene-induced fibrosarcoma
 CC cancer cells from mice. Cancer associated antigens and a pharmacoma
 CC composition containing nucleic acid molecules encoding cancer associated
 CC antigens are used to treat a condition e.g. cancer. Cancer associated
 CC pharmaceutical compositions comprising them, antibodies against them and the
 CC monitoring and treating the diseases characterized by the expression of
 CC one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for
 CC research purposes. Cancer associated antigens DNA is also useful in gene
 CC therapy. The present sequence is a cDNA encoding human cancer associated
 CC antigen OY-TES-1
 XX
 XX Sequence 1895 BP; 449 A; 565 C; 481 G; 400 T; 0 U; 0 Other;

Query Match 100.0%; Score 1895; DB 5; Length 1895;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GTTAGAGGCGGCTTGTGTCACAGGACGCGGCGGATCTTCCGGCCATGAGAACCA 60
 OY 61 GCGGCTGGCTTCTCTCCCTCACTCTGAGAGGCTGCTCCGCTTGGCACTGGCCGCA 120
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 OY 1141 GGGGCGGACACATGCTTACTGTGCTCTGTGACCTTCTGTAAGCTGAGAGAG 1200
 Db 1141 GGGGCGGACACATGCTTACTGTGCTCTGTGACCTTCTGTAAGCTGAGAGAG 1200
 OY 1201 TGCCACTCAGAGGCGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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 OY 1621 GAGCTGTGCTTGTGATGAGAGCAGAGAGTTCAAGCACTTGAAGCAGTTCGATGA 1680

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Qy      1741 ACCCATTTGCTTTCAGAGCTGCCCCCTTGTGGTCTGTATTCTGGGCCCTTACTCATTTCC 1800
Db      1741 ACCCATTTGCTTTCAGAGCTGCCCCCTTGTGGTCTGTATTCTGGGCCCTTACTCATTTCC 1800
Qy      1801 TTGGGTTGAGCAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGGCTTCTTAAAGA 1860
Db      1801 TTGGGTTGAGCAACAGTCCCAAGAGAGGCGCAGGTGGAGCTGCGGCTTCTTAAAGA 1860
Qy      1861 TGACTTTACATAAATGTGTGATCTTCAAAAAA 1895
Db      1861 TGACTTTACATAAATGTGTGATCTTCAAAAAA 1895

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RESULT 2

AAZ50927 standard; cDNA; 1912 BP.

AAZ50927; 05-JUN-2000 (first entry)

Human Protease and associated protein-10 (PPRG-10) encoding cDNA.

Protease and associated protein-10; PPRG-10; anti-PPRG antibody;
 diagnosis; treatment; cell proliferative disorder; cancer; cirrhosis;
 arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
 AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
 ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
 hepatocellular; antiinflammatory; virucide; antiparietal; anti-HIV;
 antiallergic; immunosuppressive; antidiabetic; antianaemic;
 neuroprotective; human; ss.

Homo sapiens.

Location/Qualifiers

Key CDS

/tag= a

/product= "Human PPRG-10"

/tag= b

/tag= c

/product= "Mature PPRG-10"

/tag= d

/bound_moiety= "Probe or Primer"

misc_binding

/tag= d

/bound_moiety= "Probe or Primer"

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PT cell proliferative disorders such as atherosclerosis.

XX Claim 9; Page 106; 114pp; English.

The present sequence is a cDNA identified in Incyte clone 1393301 derived
 from THYNOT03 cDNA library. It encodes human protease and associated
 protein-10 (PPRG-10), which is expressed in reproductive, endocrine,
 haematopoietic and immune tissues. Anti-PPRG antibodies can be used as
 therapeutic antagonists, reagents for diagnosis and monitoring diseases
 and for isolating PPRG. PPRG nucleotide sequence can be used as probe or
 primer for diagnosis and monitoring of PPRG-related diseases and gene
 mapping. PPRG can be used in the treatment of cell proliferative
 disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,
 cirrhosis and hepatitis, and immune disorders like AIDS, Addison's
 disease, adult respiratory distress syndrome, allergies, ankylosing
 spondylitis and amyloidosis

Sequence 1912 BP; 455 A; 567 C; 487 G; 403 T; 0 U; 0 Other;

Query Match 99.7%; Score 1890.2; DB 3; Length 1912;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      61 GCGCGTGGCTTCTCCCTCCCTCCTCCTGAGAGTCTGCTGCTGCGACCTGCGCGCA 120
Db      77 GCGCGTGGCTTCTCCCTCCCTCCTCCTGAGAGTCTGCTGCTGCGACCTGCGCGCA 136
Qy      121 GCCCAGAGTTCAGTCAAGCGCCCACTCCAGAGCGCTCTCTCTCAAGAAATAGAA 180
Db      137 GCCCAGAGTTCAGTCAAGCGCTCCATCCAGAGCGCTCTCTCTCAAGAAATAGAA 196
Qy      181 CGCTTCTTGCAGTCTGACTCCAACTGAGAGGACAGACTACTGCGCTTCCGTGCA 240
Db      197 CGCTTCTTGCAGTCTGACTCCAACTGAGAGGACAGACTACTGCGCTTCCGTGCA 256
Qy      241 ACCCAGCGCTGCGGAGATCCCACTCCAGAGCGCTCTCTCTCAAGAAATAGAA 300
Db      257 ACCCAGCGCTGCGGAGATCCCACTCCAGAGCGCTCTCTCTCAAGAAATAGAA 316
Qy      301 GTGCCGAGTGTGCTGCTGCTCCTCAACTCTCTTATGCTCTGTTAGTCTTCTGCG 360
Db      317 GTGCCGAGTGTGCTGCTGCTCCTCAACTCTCTTATGCTCTGTTAGTCTTCTGCG 376
Qy      361 CAGTTCACTCACTACCGTTGCTCAACACAGTCTATGCAAGAGTCTGTGTTCC 420
Db      377 CAGTTCACTCACTACCGTTGCTCAACACAGTCTATGCAAGAGTCTGTGTTCC 436
Qy      421 CAGCAGTCTCTATTCTCTCACTTAACCTCTCAAGAGATTAAGCTTCAAGTCAAG 480
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Qy      481 TCACCCAGCAGATGAGCTCCCTCCATCTCAACCTCTCAAGTCAAGAGAGTCTGAG 540
Db      497 TCACCCAGCAGATGAGCTCCCTCCATCTCAACCTCTCAAGTCAAGAGAGTCTGAG 556
Qy      541 TTCACGCTGAGCTGAGAGGCTCAGCAACAGTGAAGAGTCTTCAATCTCTCTTG 600
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Db      677 CAGAGCCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
Qy      721 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780

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Db 553 CAGCAACAACTGTGAGAGAGCTCTTCAATCTCTTGTGCTCCGGAACCCAGGAGCAGC 612
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 Qy 744 GGAAG 803
 Db 733 GGAAG 792
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 Qy 864 ACGAG 923
 Db 853 AG 912
 Qy 924 CAG 983
 Db 913 CAG 972
 Qy 984 CCGTGGAGAGCTTCTGAGAGCTGCCCCACAGAGAGCTTGTGTGTGTGTGTGTGTGTGT 1043
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 Qy 1044 CGTGAG 1103
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 Qy 1404 AGATGTCCGAGTCTGT 1463
 Db 1391 AGATGTCCGAGTCTGT 1449
 Qy 1464 CCGTACCAAGTTTGT 1523
 Db 1450 CCGTACCAAGTTTGT 1509
 Qy 1524 CAG 1583
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 Qy 1584 TGAAG 1643
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 Qy 1644 GAGGTTCAG 1703

Db 1630 GAGGTTCAG 1689
 Qy 1704 CCGAGCCCAACCTGAG 1763
 Db 1690 CCGAGCCCAACCTGAG 1749
 Qy 1764 CTTCTGGGTCTGT 1823
 Db 1750 CTTCTGGGTCTGT 1809
 Qy 1824 AG 1883
 Db 1810 AG 1868
 Qy 1884 TTCAAAAAAAA 1895
 Db 1869 TTCAAAAAAAA 1880

RESULT 6

ADAA39940 standard; cDNA, 1892 BP.

ADAA39940;

20-NOV-2003 (first entry)

Human secreted protein encoding cDNA.

KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytostatic; immunosuppressive; neuroprotective;
 KW antiviral; anticancer; hepatocellular; antidiabetic; antiinflammatory;
 KW vulnery; cardiac; gene therapy; ss.

OS Homo sapiens.

PN WO2002102993-A2.

PD 27-DEC-2002.

PF 19-MAR-2002; 2002WO-US008123.

PR 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-031287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM,

DR WPI; 2003-175238/17.

XX New human secreted proteins and nucleic acid molecules, useful for

PT preparing a diagnostic or pharmaceutical composition for

PT preventing or treating cancer or other hyperproliferative disorder,

PT asthma, allergies or AIDS.

PS Claim 9; SEQ ID NO 322; 3205BP; English.

CC The invention relates to novel genes ADAA39629-ADAA0565 and proteins
 CC ADAA0566-ADAA1501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic

CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match 95.6%; Score 1811.2; DB 8; Length 1892;

Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY 24 GGAAGCGGGGATCTTCTCCGGCATGAGGAAGCCAGCGCTGCTTCTTCCCTCACT 83
 Db 13 GGAAGCGGAGCGATCTTCTCCGGCATGAGGAAGCCAGCGCTGCTTCTTCCCTCACT 72
 QY 84 CCTGAAGGTCCTCTGCTGCTGCACTGCGGAGCCAGAGTTCCGACTAGAGCCC 143
 Db 73 CCTGAAGGTCCTCTGCTGCTGCACTGCGGAGCCAGAGTTCCGACTAGAGCCC 132
 QY 144 CACTCCAGGAGCGCTCTCTCTCTACCGAATAGAAAGCTTCTTGCACTGCTGACTCC 203
 Db 133 CACTCCAGGAGCGCTCTCTCTCTACCGAATAGAAAGCTTCTTGCACTGCTGACTCC 192
 QY 204 AACCTGGAAGGAGAGACTAAGTCCGCTCTCGGTGCAACCCAGCGCTGCGGAATCCAC 263
 Db 193 AACCTGGAAGGAGAGACTAAGTCCGCTCTCGGTGCAACCCAGCGCTGCGGAATCCAC 252
 QY 264 ACTCGTCGAGCTGGAACCAATATGAAAAACAGGCTTAAGTCCGAGTGTCTGTCTC 323
 Db 253 ACTCGTCGAGCTGGAACCAATATGAAAAACAGGCTTAAGTCCGAGTGTCTGTCTC 312
 QY 324 CAACCTCCCTTATGCTCTCTGTTGAGTCTTCTGCAAGTCACTACAGCTTGTCTC 383
 Db 313 CAACCTCCCTTATGCTCTCTGTTGAGTCTTCTGCAAGTCACTACAGCTTGTCTC 372
 QY 384 CAACCACTGCTACTATGCAAGAGAGTCTGTGTCTCCAGCAAGTCTTATTTCTTACC 443
 Db 373 CAACCACTGCTACTATGCAAGAGAGTCTGTGTCTCCAGCAAGTCTTATTTCTTACC 432
 QY 444 TTAACATCTTCAGAGAAATGAAAGCTTCAAGTGAAGTCAACCAACCAATGACTCTCC 503
 Db 433 TTAACATCTTCAGAGAAATGAAAGCTTCAAGTGAAGTCAACCAACCAATGACTCTCC 492
 QY 504 CATCTCAACCCATTCAAGTGAAGAGCCAGACCTTCCAGGCGCTGAGAGGCT 563
 Db 493 CATCTCAACCCATTCAAGTGAAGAGCCAGACCTTCCAGGCGCTGAGAGGCT 552
 QY 564 CAGCAACCAAGTGAAGAGTCTTACATCTTGTCTGAGAGGCGAGAGCAAGC 623
 Db 553 CAGCAACCAAGTGAAGAGTCTTACATCTTGTCTGAGAGGCGAGAGCAAGC 612
 QY 624 GCCAGAGCAACAGAGAGAGAGTGAAGCAGAGCAGAGAACCCACAAAGAACAA 683
 Db 613 GCCAGAGCAACAGAGAGAGAGTGAAGCAGAGCAGAGAACCCACAAAGAACAA 672
 QY 684 GCAGGAAGAGGGGCAAAAACAGGAAGAGCAAGGAAGGAACAGGAAGAGGGAAGCA 743
 Db 673 GCAGGAAGAGGGGCAAAAACAGGAAGAGCAAGGAAGGAACAGGAAGAGGGAAGCA 732
 QY 744 GGAAGGAAGGACAGGGGACTAAGAGGAGCGGAGGCTGTGTCTCACTGACAGACAGCTC 803
 Db 733 GGAAGGAAGGACAGGGGACTAAGAGGAGCGGAGGCTGTGTCTCACTGACAGACAGCTC 792
 QY 804 AGAGCCCAAGTTTCACTGTAATCTATCTTAAACCTTCTTCTTCTCCCGGGT 863
 Db 793 AGAGCCCAAGTTTCACTGTAATCTATCTTAAACCTTCTTCTTCTCCCGGGT 852
 QY 864 ACAGGAAGTGAAGTCTACTCTATGATATGAGAAACATCCAGAGCTCATTCATCAGC 923
 Db 853 ACAGGAAGTGAAGTCTACTCTATGATATGAGAAACATCCAGAGCTCATTCATCAGC 912
 QY 924 CCAGGAATATGATGAATGAATGAATATATATGATGGAAGTCTTACTGAGAAACCAAAA 983
 Db 913 CCAGGAATATGATGAATGAATGAATATATATGATGGAAGTCTTACTGAGAAACCAAAA 972
 QY 984 CCTGAGAGCTTCTGAGAGTCCCAACAGAGGCTTGTGATGATGATGAT 1043
 Db 973 CCTGAGAGCTTCTGAGAGTCCCAACAGAGGCTTGTGATGATGATGATGAT 1031
 QY 1044 CCGTGAAGATACCTGATCATTAACCCCAAGCCAGGCTGGAAGTACATGAGAGAGA 1103
 Db 1032 CCGTGAAGATACCTGATCATTAACCCCAAGCCAGGCTGGAAGTACATGAGAGAGA 1091
 QY 1104 GATCTTGGTTTGGGAAGTCCGTCTGTGACAGCTTGGGCGGCGACATGTCTACTG 1163
 Db 1092 GATCTTGGTTTGGGAAGTCCGTCTGTGACAGCTTGGGCGGCGACATGTCTACTG 1151
 QY 1164 TGCCCTCTGATCTTGTGCTCTTGAAGCTGAGAGTGCACATGACAGGCGCAGCTGCA 1223
 Db 1152 TGCCCTCTGATCTTGTGCTCTTGAAGCTGAGAGTGCACATGACAGGCGCAGCTGCA 1211
 QY 1224 GCGGCAACATGCGAGACCTCCCAAGAGCTCCCTTGTGACAGCCCTTGTGCTCCCA 1283
 Db 1212 GCGGCAACATGCGAGACCTCCCAAGAGCTCCCTTGTGACAGCCCTTGTGCTCCCA 1270
 QY 1284 GAGCTGTTCATGCGCAACAGGATAGGTCGCCAAGTCAAGGCGCTTTTACGGGCTGA 1343
 Db 1271 GAGCTGTTCATGCGCAACAGGATAGGTCGCCAAGTCAAGGCGCTTTTACGGGCTGA 1330
 QY 1344 TTTGTAGGATGGGCTCAATGAGACTTGTGTGTCGGGCTTGGCAAGGAGGCTGTGA 1403
 Db 1331 TTTGTAGGATGGGCTCAATGAGACTTGTGTGTCGGGCTTGGCAAGGAGGCTGTGA 1390
 QY 1404 AGATGTCCAGAGTCTCGGGTGTGCTCCAGACTGAGTCTTACAGATGGGAGTTT 1463
 Db 1391 AGATGTCCAGAGTCTCGGGTGTGCTCCAGACTGAGTCTTACAGATGGGAGTTT 1449
 QY 1464 CCTTCAAGATTTTGAACAAGACTATATCCAGTACCAAACTACTGTTCTTCAAAAG 1523
 Db 1450 CCTTCAAGATTTTGAACAAGACTATATCCAGTACCAAACTACTGTTCTTCAAAAG 1509
 QY 1524 CCAAGAGTGTGATGAGAAACCGCAATGGAAGGATCCCGATGATGATGTCTGAGAA 1583
 Db 1510 CCAAGAGTGTGATGAGAAACCGCAATGGAAGGATCCCGATGATGATGTCTGAGAA 1569
 QY 1584 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAAGTGAAGAGTGTGCTTGAAGAGCA 1643
 Db 1570 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAAGTGAAGAGTGTGCTTGAAGAGCA 1629
 QY 1644 GGAATTCAGACCTTGAAGTCTTGAAGGAGTTCGAGTGTGAGTCTATTTCTGCCACAC 1703
 Db 1630 GGAATTCAGACCTTGAAGTCTTGAAGGAGTTCGAGTGTGAGTCTATTTCTGCCACAC 1689
 QY 1704 CCGAGCCCAACCTGCGCAAGTCTTATGTTTGAAGCCCAATTCCTTCAAGGCTGCCC 1763
 Db 1690 CCGAGCCCAACCTGCGCAAGTCTTATGTTTGAAGCCCAATTCCTTCAAGGCTGCCC 1749
 QY 1764 CTTCTGGGCTCTGTTACTCGGCTTCACTCAATTTCTTGGTTTGAAGCAACAGTCCAG 1823
 Db 1750 CTTCTGGGCTCTGTTACTCGGCTTCACTCAATTTCTTGGTTTGAAGCAACAGTCCAG 1809
 QY 1824 AGAGGGCCACGGTGGAGCTGGGCTCTTAAAGATGACTTTACATTAATGTTGATC 1883
 Db 1810 AGAGGGCCACGGTGGAGCTGGGCTCTTAAAGATGACTTTACATTAATGTTGATC 1868

QY 1894 TTCAAAAAAAAA 1895
 DB 1869 TTCAAAAAAAAA 1880

RESULT 7

ID ADC73578 standard; DNA; 1892 BP.

AC ADC73578;

DT 01-JAN-2004 (first entry)

DE Human secreted protein-related DNA - SEQ ID 211.

antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
 antiidiabetic; immunosuppressive; dermatological; nephrotoxic;
 antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
 fungicide; antiparasitic; antierosive; antidiabetic; cytostatic;
 haemopoietic; haematologic; anaemia; autoimmune disorder;
 rheumatoid arthritis; inflammation; Grave's disease; diabetes;
 systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
 Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
 cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
 human; gene; ds.

OS Homo sapiens.

XX MO200308063-A2.

PD 08-MAY-2003.

PF 19-MAR-2002; 2002MO-US008277.

PR 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI; 2003-430516/40.

DR P-PSDB; ADC74193.

PT New human secreted polypeptide for diagnosing, preventing or treating

PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune

PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or

PT atherosclerosis).

PS Claim 27; SEQ ID NO 211; 2272bp; English.

XX The invention relates to a novel human secreted polypeptide comprising a
 CC defined sequence given in the specification. The polypeptide, nucleic
 CC acid molecule, antibody, agonist or antagonist of the invention may be
 CC useful for preparing a composition for diagnosing or treating a
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune
 CC disorders or rheumatoid arthritis, inflammation, Grave's disease,
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
 CC disease, wounds and hyperproliferative disorders including
 CC parasitic infections, as well as bacterial, viral, fungal or
 CC therapy procedures and for identifying a binding partner by contacting
 CC the polypeptide with a binding partner and determining whether the
 CC binding partner increases or decreases the activity of the polypeptide.
 CC The current sequence is that of the human secreted protein-related DNA of
 CC the invention.

SQ Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match

95.6%; Score 1811.2; DB 10; Length 1892;

Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY	24	GGACGGGGGGGATCTTCTCGGCAATGAGAAAGCCGCGCTTCTCCGCACT	83
DB	13	GGACCGGAGGATCTTCTCGGCAATGAGAAAGCCGCGCTTCTCCGCACT	72
QY	84	CTTGAAGGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	143
DB	73	CTTGAAGGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	132
QY	144	CATCTCAGGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	203
DB	133	CATCTCAGGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	192
QY	204	AACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	263
DB	193	AACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	252
QY	264	ACTGCTCAGCTGAGCAATATGAAACCAAGGCTTATGCGGATGCTGCTGCT	323
DB	253	ACTGCTCAGCTGAGCAATATGAAACCAAGGCTTATGCGGATGCTGCTGCT	312
QY	324	CAACCTCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	383
DB	313	CAACCTCCCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	372
QY	384	CAACCACTCTATCTATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	443
DB	373	CAACCACTCTATCTATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	432
QY	444	TAACTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	503
DB	433	TAACTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	492
QY	504	CATCTCAGCTGAGCAATATGAAACCAAGGCTTATGCGGATGCTGCTGCT	563
DB	493	CATCTCAGCTGAGCAATATGAAACCAAGGCTTATGCGGATGCTGCTGCT	552
QY	564	CAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	623
DB	553	CAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	612
QY	624	GCCAGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	683
DB	613	GCCAGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	672
QY	684	GCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	743
DB	673	GCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	732
QY	744	GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	803
DB	733	GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	792
QY	804	AGAGCCCAAGTTCACTGTAATCTCTATCTCTTCAACCTTCTCTTCTCT	863
DB	793	AGAGCCCAAGTTCACTGTAATCTCTATCTCTTCAACCTTCTCTTCTCT	852
QY	864	ACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	923
DB	853	ACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	912
QY	924	CCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	983
DB	913	CCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	972
QY	984	CCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1043
DB	973	CCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1031
QY	1044	CGTGAAGATACCTGATCATATACCCCAAGGAGGAGGAGGAGGAGGAGGAG	1103

Db 1032 CGTGAGAAATCTGCATCAATACCCCAAGCCCTGGAAGTACATGAGAGGA 1091
 QY 1104 GATCCTTGTGTTGGGAAAGTGGTCTGTGACAGCCTTGGGGGACACATGTTCTACCTG 1163
 Db 1092 GATCCTTGTGTTGGGAAAGTGGTCTGTGACAGCCTTGGGGGACACATGTTCTACCTG 1151
 QY 1164 TGCCTCTGTGACTTCTGCTCTTTGAAGCTGAGACAGTGCCTCAGAGGCCAGCCTGCA 1223
 Db 1152 TGCCCTCTGTGACTTCTGCTCTTTGAAGCTGAGACAGTGCCTCAGAGGCCAGCCTGCA 1211
 QY 1224 GGGGCAACAATGAGCAACCTCCCAAGAGATCCCTTTGTAGAGCCCTTGTGCTCCCA 1283
 Db 1212 GGGGCAACAATGAGCAACCTCCCAAGAGATCCCTTTGTAGAGCCCTTGTGCTCCCA 1270
 QY 1284 GAGCCTGTCCATGAGCAACAGGATAGGATCCCAAGATCAGGCGCTTTTACGGGCTGGA 1343
 Db 1271 GAGCCTGTCCATGAGCAACAGGATAGGATCCCAAGATCAGGCGCTTTTACGGGCTGGA 1330
 QY 1344 TTTGTACGTTGGGCTCCACATGACATTTCTGTGTGCTCCGCTTTGCCACGAAAGCTGTGA 1403
 Db 1331 TTTGTACGTTGGGCTCCACATGACATTTCTGTGTGCTCCGCTTTGCCACGAAAGCTGTGA 1390
 QY 1404 AGATGTCCTGATCTGTGGTGGTCTCCAGATGAGTCTTACGTTCCAGATGGGATTT 1463
 Db 1391 AGATGTCCTGATCTGTGGTGGTCTCCAGATGAGTCTTACGTTCCAGATGGGATTT 1449
 QY 1464 CCTTACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAG 1523
 Db 1450 CCTTACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAG 1509
 QY 1524 CCAGCAGTGTCTGATGAGAAACCGCAATCGAAAGTGTCCGATGAGATGTCTGCAGAA 1583
 Db 1510 CCAGCAGTGTCTGATGAGAAACCGCAATCGAAAGTGTCCGATGAGATGTCTGCAGAA 1569
 QY 1584 TGAAGACTTACAGTGGCTGTGAGCCCTGGCAAAAGTGAAGAGTGTGTTGATGAGAGCCA 1643
 Db 1570 TGAAGACTTACAGTGGCTGTGAGCCCTGGCAAAAGTGAAGAGTGTGTTGATGAGAGCCA 1629
 QY 1644 GGAATTCAGACCTTACTCTAGTCCAGATTCGATGAGCTGAGGCTTATCTGCCCCAC 1703
 Db 1630 GGAATTCAGACCTTACTCTAGTCCAGATTCGATGAGCTGAGGCTTATCTGCCCCAC 1689
 QY 1704 CCAGGCCCAACCTGCCACAGTCTCTATGTTTGAAGACCCCATGCTTCAAGCTGCC 1763
 Db 1690 CCAGGCCCAACCTGCCACAGTCTCTATGTTTGAAGACCCCATGCTTCAAGCTGCC 1749
 QY 1764 CTTTGGGCTGTGTTACTCGGCCCCCTTACTACATTTCTTGGGTTGAAGACAGCTCCAG 1823
 Db 1750 CTTTGGGCTGTGTTACTCGGCCCCCTTACTACATTTCTTGGGTTGAAGACAGCTCCAG 1809
 QY 1824 AGAGGGCCACGAGTGGAGCTGGCCCTTAAAGATGACTTACATTAATGTTGATC 1883
 Db 1810 AGAGGGCCACGAGTGGAG-TCGCGCCCTCTTAAAGATGACTTACATTAATGTTGATC 1868
 QY 1884 TTCAAAAA 1895
 Db 1869 TTCAAAAA 1880
 RESULT 8
 ADD37623
 ID ADD37623 standard; cDNA; 1892 BP.
 XX
 AC ADD37623;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human secreted protein encoding sequence #105.
 XX
 KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
 XX
 OS Homo sapiens.

XX
 PN WO200290526-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008279.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WFI; 2003-140218/13.
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 PT treating allergic or asthmatic disorders, or related immediate
 PT hypersensitivity disorders.
 XX
 PS Claim 7; SEQ ID NO 105; 1323bp; English.
 XX
 CC The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful
 CC for identifying a binding partner by contacting the polypeptide with a
 CC binding partner, and determining whether the binding partner increases or
 CC decreases the activity of the polypeptide. The polypeptides and nucleic
 CC acid molecules are also useful for detecting, preventing, diagnosing,
 CC prognosticating, treating or ameliorating inflammatory disorders
 CC neoplastic diseases, wound healing and disorders of epithelial cell
 CC proliferation, immune disorders, cardiovascular disorders, blood-related
 CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
 CC disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping, as molecular weight markers, or as hybridization or diagnostic
 CC probes. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The present sequence represents a human
 CC secreted protein encoding sequence.
 XX
 SO Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
 Query Match 95.6%; Score 1811.2; DB 10; Length 1892;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
 QY 24 GGAAGCGGGCGGATCTTCTCCGGCCATGAGAAAGCCAGCCGCTTCTCCCTCACT 83
 Db 13 GGAAGCGGACGAGATCTTCTCCGGCCATGAGAAAGCCAGCCGCTTCTCCCTCACT 72
 QY 84 CCTGAAGTGTGCTCTGCTCTGTGACCTGGACCTGGCCAGGATTCAGTCAAGGCC 143
 Db 73 CCTGAAGTGTGCTCTGCTCTGTGACCTGGACCTGGCCAGGATTCAGTCAAGGCC 132
 QY 144 CACTCCAGGACGCTCTCTCTCTTACCGAATACGAACCTTTCGACATGCTGACTCC 203
 Db 133 CACTCCAGGACGCTCTCTCTCTTACCGAATACGAACCTTTCGACATGCTGACTCC 192
 QY 204 AACCTGGAAGGACGAGACTACTGCGCTCTCGGTGACACCCAGGCTGCCGAATCCAC 263
 Db 193 AACCTGGAAGGACGAGACTACTGCGCTCTCGGTGACACCCAGGCTGCCGAATCCAC 252
 QY 264 ACTCGTCAGCTGAGCAATATGAAAAACAGGCTTAGGCCGATGAGTGTGCTC 323
 Db 253 ACTCGTCAGCTGAGCAATATGAAAAACAGGCTTAGGCCGATGAGTGTGCTC 312
 QY 324 CAACTCCCTTATGCTCTGAGTGTGAGTCTTTCGCAAGTTCACTCACTACCGTGTCTC 383

Db 313 CAACCTCCCTTATGCTCCCTGCTTGAAGTCTTTCTTCCGAGTTCACTGACTACCGTGTCTC 372
 Qy 384 CAACCAAGTCTACTATGCGCAAGAGATCTGTGTCTCCAGCGACTCTCTATTCTTCACC 443
 Db 373 CAACCAAGTCTACTATGCGCAAGAGATCTGTGTCTCCAGCGACTCTATTCTTCACC 443
 Qy 444 TAACTCTCAAGAGATAGAAAGCTTCACTGAAAGTCTCAACCAAGATGACTCTCC 432
 Db 433 TAACTCTCAAGAGATAGAAAGCTTCACTGAAAGTCTCAACCAAGATGACTCTCC 432
 Qy 504 CATCTCACCCCACTTCAAGTACAGCAAGCCGAGACTTCCAGCCCTGAGCGCTGAGAGCT 563
 Db 493 CATCTCACCCCACTTCAAGTACAGCAAGCCGAGACTTCCAGCCCTGAGCGCTGAGAGCT 552
 Qy 564 CAGCAACACGCTGGAAGAGCTCTTCAATCTCTCTGTCTCTGAGAGCGCAAGAGAGCT 623
 Db 553 CAGCAACACGCTGGAAGAGCTCTTCAATCTCTCTGTCTCTGAGAGCGCAAGAGAGCT 612
 Qy 624 GCCAGACACAGAGAGAGAGAGAGTGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 672
 Db 613 GCCAGACACAGAGAGAGAGAGAGTGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 672
 Qy 684 GCAAGAAAG 743
 Db 673 GCAAGAAAG 732
 Qy 744 GGAAGAAAG 803
 Db 733 GGAAGAAAG 792
 Qy 804 AGAGCCCAAGTTTCACTGAACTCTTATCTTCTTAACTCTCTCTCTCTCTCTCTCTCT 863
 Db 793 AGAGCCCAAGTTTCACTGAACTCTTATCTTCTTAACTCTCTCTCTCTCTCTCTCTCT 852
 Qy 864 ACGAGAGTAGAGTCTACTCTCTATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAG 923
 Db 853 ACGAGAGTAGAGTCTACTCTCTATGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
 Qy 924 CAGAGAAATAGATGAATGAATGAATTAATGATGAAGAGAGAGAGAGAGAGAGAGAG 983
 Db 913 CAGAGAAATAGATGAATGAATGAATTAATGATGAAGAGAGAGAGAGAGAGAGAGAG 972
 Qy 984 CCCGCGAGCTTCTCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
 Db 973 CCCGCGAGCTTCTCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
 Qy 1044 CGTGAAGAAATCTGATCATTAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
 Db 1032 CGTGAAGAAATCTGATCATTAATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
 Qy 1104 GATCTCTGAGTTCGGAGAGTGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163
 Db 1092 GATCTCTGAGTTCGGAGAGTGTGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
 Qy 1164 TGCCCTCTGTGACTTCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
 Db 1152 TGCCCTCTGTGACTTCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1211
 Qy 1224 GCGGCAACAATGAG 1283
 Db 1212 GCGGCAACAATGAG 1270
 Qy 1284 GAGCTGTCCATGCGCAACAGGTAGAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1343
 Db 1271 GAGCTGTCCATGCGCAACAGGTAGAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1330
 Qy 1344 TTTGTACGAGTGGCTCAATGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1403
 Db 1331 TTTGTACGAGTGGCTCAATGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1390
 Qy 1404 AGATGTCAGAGTCTGT 1463
 Db 1391 AGATGTCAGAGTCTGT 1449

Qy 1464 CCTTACCAAGATTGTGACAGAGACTATTCAGTACCCAACTACTGTCTTCAAAAG 1523
 Db 1450 CCTTACCAAGATTGTGACAGAGACTATTCAGTACCCAACTACTGTCTTCAAAAG 1509
 Qy 1524 CCAGAGAGTCTGATGAGAAACCGCAATCGGAAGTGTCCCGCATGAGATGTCTGAGAA 1583
 Db 1510 CCAGAGAGTCTGATGAGAAACCGCAATCGGAAGTGTCCCGCATGAGATGTCTGAGAA 1569
 Qy 1584 TGAGCTTACAGTCCGCTGAGAGCCCTGCAAAAAGTGAAGAGAGCTTGTCTTCATGAGCA 1643
 Db 1570 TGAGCTTACAGTCCGCTGAGAGCCCTGCAAAAAGTGAAGAGAGCTTGTCTTCATGAGCA 1629
 Qy 1644 GGAATTGAGAGAGCTTGAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
 Db 1630 GGAATTGAGAGAGCTTGAAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689
 Qy 1704 CCCAGCCCAACTGAGAGAGTCTCTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
 Db 1690 CCCAGCCCAACTGAGAGAGTCTCTATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1749
 Qy 1764 CTTCTGAGTCTGTGCTGAG 1823
 Db 1750 CTTCTGAGTCTGTGCTGAG 1809
 Qy 1824 AGAGAGCCAGCTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
 Db 1810 AGAGAGCCAGCTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1868
 Qy 1884 TTCAAAAAATAA 1895
 Db 1869 TTCAAAAAATAA 1880

RESULT 9
 ADA56130
 ID ADA56130 standard; DNA; 1892 BP.
 AC ADA56130;
 XX
 DT 20-NOV-2003 (first entry)
 DE
 XX
 KW Gene encoding human secreted protein #309.
 DE
 KW immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
 KW cytostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antihypertensive; antidiabetic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology; ds;
 gene.
 XX
 OS Homo sapiens.
 XX
 PN MO200210294-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 XX
 PR 19-JUL-2001; 2001US-0306171P.
 XX
 PR 13-NOV-2001; 2001US-0331287P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX
 XX MPI; 2003-167512/16.
 DR P-PSDB; ADA57026.

XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.

PS Claim 21; SEQ ID NO 319; 1754bp; English.

XX
CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.

XX
SQ Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;

Query Match 95.6%; Score 1811.2; DB 10; Length 1892;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
QY 24 GAGCGGGGCGGATCTTCCGSCATGAGAGAGCCAGCGGTGCTTCTCCCTCACT 83
DB 13 GGGACCGGACGATCTTCCGSCATGAGAGAGCCAGCGGTGCTTCTCCCTCACT 72
QY 84 CCTGAAGTGTGCTCTGCTCTGACCTGCGAGCCAGAGATTCAGTCAAGGCC 143
DB 73 CCTGAAGTGTGCTCTGCTCTGACCTGCGAGCCAGAGATTCAGTCAAGGCC 132
QY 144 CACTCCAGGAGCGCTCTCTCTCAACGAAATGAAAGCTTTTGCACTGCTGACTC 203
DB 133 CACTCCAGGAGCGCTCTCTCTCAACGAAATGAAAGCTTTTGCACTGCTGACTC 192
QY 204 AACCTGAAAGGAGAGACTACCTGCGCTCCGATGAAACCGAGGTCGCGGAATCCAC 253
DB 193 AACCTGAAAGGAGAGACTACCTGCGCTCCGATGAAACCGAGGTCGCGGAATCCAC 252
QY 264 ACTCGTCAGCTGAGCAATATGAAAAACAAGCTTAGTCCGAGTGTGCTGCTC 323
DB 253 ACTCGTCAGCTGAGCAATATGAAAAACAAGCTTAGTGTGCTGCTGCTGCTC 312
QY 324 CAACCTCCCTTATGCTCTCTGTTTGAAGTTTCTTGTGCACTCACTACGTTGCTC 383
DB 313 CAACCTCCCTTATGCTCTCTGTTTGAAGTTTCTTGTGCACTCACTACGTTGCTC 372
QY 384 CAACCACTCTATGAGCAAGAGTCTGTGTTCCAGCAGTCTCTATTCCTCAAC 443
DB 373 CAACCACTCTATGAGCAAGAGTCTGTGTTCCAGCAGTCTCTATTCCTCAAC 442
QY 444 TAACTCTCTAAGGAGATGAAAGCTTCACTGAAGTCTCAACCAAGTGAAGCTTCCC 503

DB 433 TAACTCTCTAAGGAGATGAAAGCTTCACTGAAGTCTCAACCAAGTGAAGCTTCCC 492
QY 504 CATCTCAACCCCACTTCAAGTGAAGAGCCAGAGCTTCCAGGCTGGCTGAGAGCT 563
DB 493 CATCTCAACCCCACTTCAAGTGAAGAGCCAGAGCTTCCAGGCTGGCTGAGAGCT 552
QY 564 CAGCAACAGTGAAGAGCTCTCAATCTCTTGTCTCCCTGGAGCCAGAGCAAGC 623
DB 553 CAGCAACAGTGAAGAGCTCTCAATCTCTTGTCTCCCTGGAGCCAGAGCAAGC 612
QY 624 GCCAGAGCAACAGAGAGGAGAGTGTGACACAGGCAAGAGCCAGCAAGACAA 683
DB 613 GCCAGAGCAACAGAGAGGAGAGTGTGACACAGGCAAGAGCCAGCAAGACAA 672
QY 684 GCAGGAAGAGGAG 743
DB 673 GCAGGAAGAGGAG 732
QY 744 GGAAGAAAG 803
DB 733 GGAAGAAAG 792
QY 804 AGAGCCCAAGTTTCACTGATCTCTATCTTAACTCTTCTCTTCTCTCCGAGT 863
DB 793 AGAGCCCAAGTTTCACTGATCTCTATCTTAACTCTTCTCTCTCTCCGAGT 852
QY 864 ACAGAGAGTGAATCTCTATCTCTATGTAATGAGAAATCCAGAGAGTCAATGAG 923
DB 853 ACAGAGAGTGAATCTCTATCTCTATGTAATGAGAAATCCAGAGAGTCAATGAG 912
QY 924 CCAGAAATGATGAATGAATGAATATATATGAGAACTCTCACTGAGAAACCAAA 983
DB 913 CCAGAAATGATGAATGAATGAATATATATGAGAACTCTCACTGAGAAACCAAA 972
QY 984 CCCTGAGCTTCTCTGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043
DB 973 CCCTGAGAGCTCTCTGAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
QY 1044 CCGAGAGATTAATCTGATCATATACCCCAAGGCAAGGCTTGAAGTATGAGAGAG 1103
DB 1032 CCGAGAGATTAATCTGATCATATACCCCAAGGCAAGGCTTGAAGTATGAGAGAG 1091
QY 1104 GATCTTGTGTTGGGAAAGTGGTCTGTGACAGCTTGGGCGGAGCAATGCTACTG 1163
DB 1092 GATCTTGTGTTGGGAAAGTGGTCTGTGACAGCTTGGGCGGAGCAATGCTACTG 1151
QY 1164 TGCCTCTGTGACTTCTGCTCTTGAAGCTGAGAGAGTCACTCAAGAGCCAGCTGCA 1223
DB 1152 TGCCTCTGTGACTTCTGCTCTTGAAGCTGAGAGAGTCACTCAAGAGCCAGCTGCA 1211
QY 1224 GCGGCAACATGAGCACTCCCAAGAGTCCCTTTGTGAGCCCTTGTGCTTCCCA 1283
DB 1212 GCGGCAACATGAGCACTCCCAAGAGTCCCTTTGTGAGCCCTTGTGCTTCCCA 1270
QY 1284 GAGCTGTCCATGAGCAACAGGTAGAGTCCCAAGTCAAGGCGCTTTTAAAGGGGCTGGA 1343
DB 1271 GAGCTGTCCATGAGCAACAGGTAGAGTCCCAAGTCAAGGCGCTTTTAAAGGGGCTGGA 1330
QY 1344 TTTGTACGATGGGCTCAATGAGCTTGTGTGTGCTCCGCTTTGCCAGAAAGCTGTGA 1403
DB 1331 TTTGTACGATGGGCTCAATGAGCTTGTGTGTGCTCCGCTTTGCCAGAAAGCTGTGA 1390
QY 1404 AGATGTCCAGATCTTGTGTGTGCTCCAGACTAGATTTCTTACCTCAAGATGGGATTT 1463
DB 1391 AGATGTCCAGATCTTGTGTGTGCTCCAGACTAGATTTCTTACCTCAAGATGGGATTT 1449
QY 1464 CCTTACCAAGATTTGAGACAGACTATATCCAGTACCCAACTAATGTTCTTCAAAAG 1523
DB 1450 CCTTACCAAGATTTGAGACAGACTATATCCAGTACCCAACTAATGTTCTTCAAAAG 1509
QY 1524 CCAAGAGTGTCTGATGAGAAACCGCAATGAGAGGTGTCCCGATGATGATGTCAGAA 1583

(EVAN/) EVANS C.

The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides can be used to express recombinant proteins for analysis, characterisation or therapeutic use, as markers for tissues in which the corresponding protein is expressed, as molecular weight markers on Southern gels, as chromosome markers or tags to identify chromosomes or to map related gene positions, to compare with endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related DNA sequences, as a source of information to derive PCR primers for genetic fingerprinting, to raise anti-protein antibodies and in gene therapy. The proteins can be used to raise antibodies or to elicit another immune response, as reagents in assays designed to quantitatively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed and to treat autoimmune disorders (e.g. multiple sclerosis), systemic lupus erythematosus, insulin dependent diabetes mellitus or graft-versus-host disease), anaemias, periodontal diseases, bone fractures, cartilage damage, central nervous system disorders (e.g. Alzheimer's disease or Parkinson's disease) and cancers. The proteins and polynucleotides are also useful as nutritional sources or supplements, e.g. as carbon, nitrogen or carbohydrate sources. This sequence represents a human polynucleotide of the invention.

356 ACTCACTACCGTGCCTCCAAACCAAGTTACTATACCCTACCATCCTGCTGGT

QY 427 GTCTCTATTTCTTCACCTTAACACTCTCAAGAGATAGAGCTTCAAGTCTCAACC 486
 Db 415 GTCTCTATTTCTTCACCTTAACACTCTCAAGAGATAGAGCTTCAAGTCTCA-CC 473
 QY 487 ACCACGATGACCTTCCCATCTTCACTTCACTGACAGAAAGCCAGACTTCTCAG 546
 Db 474 ACCACGATGACCTTCCCATCTTCACTTCACTGACAGAAAGCCAGACTTCTCAG 532
 QY 547 CCTGTGCTGAGAGGCTCAGCAACAGTGGAGAGCTCTCAATCTCTTGTCCCTG 606
 Db 533 CCTGTGCTGAGAGGCTCAGCAACAGTGGAGAGCTCTCAATCTCTTGTCCCT- 591
 QY 607 GAGAGCCAGAGCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 666
 Db 592 GAGAGCCAGAGCAAGCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 650
 QY 667 CCGACACAAAGAAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 726
 Db 651 CCGACACAAAGAAACAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 709
 QY 727 GAAGAGAGGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 786
 Db 710 GAAGAGAGGAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 768
 QY 787 CAGCTGCAAGCAGACTCAGAGCCCAAGTTTCACTTGAATCTCTATCTTAACTTCC 846
 Db 769 CAGCTGCAAGCAGACTCAGAGCCCAAGTTTCACTTGAATCTCTATCTTAACTTCC 827
 QY 847 TCTTTTGGCTCCCGGGTACGAAAGTGAAGTCTTCTCTATGATATGAGAAATCCAG 906
 Db 828 TCTTTTGGCTCCCGGGTACGAAAGTGAAGTCTTCTCTATGATATGAGAAATCCAG 886
 QY 907 GAGCTCATTCGATCAGGCCAGAAATAGATGAATGAATGAATGAATGAATGAATCC 966
 Db 887 GAGCTCATTCGATCAGGCCAGAAATAGATGAATGAATGAATGAATGAATGAATCC 945
 QY 967 TACTGAGAAACCAAAACCTTGGCAGCTTCTTGCAGCTGCCCCACAGAGGCTTGTG 1026
 Db 946 TACTGAGAAACCAAAACCTTGGCAGCTTCTTGCAGCTGCCCCACAGAGGCTTGTG 1003
 QY 1027 GTGCTGTCTATTCGATCGTGAAGATACCTGCATCATTAACCCCAAGCCAGGCTTGG 1086
 Db 1004 GTGCTGTCTATTCGATCGTGAAGATACCTGCATCATTAACCCCAAGGAGGCTT- 1061
 QY 1087 AAGTATAGAGAGAGAGATCTTGTGTTGGAGAGTCCGTCTGTGACACCTTGGGCGG 1146
 Db 1062 AAGTATAGAGAGAGAGATCTTGTGTTGGAGAGTCCGTCTGTGACACCTTGGGCG- 1119
 QY 1147 CGACACATGTCTACTGTGCTCTGTGACTTCTGTGCTCTTGAAGCTGAGCAGTGCAC 1206
 Db 1120 CGACACATGTCTACTGTGCTCTGTGACTTCTGTGCTCTTGAAGCTGAGCAGTGC- 1177
 QY 1207 TCAGAGGCCAGCTGCAAGCGGCAACAATGCGACCTCCCAACAAGACTTCCCTTGTGAGC 1266
 Db 1178 TCAGAGGCCAGCTGCAAGCGGCAACAATGCGACCTCCCAACAAGACTTCCCTTGTGCA- 1235
 QY 1267 CCTTGTGCTGCTCCCAAGAGCTTGCATGCGGCAACAAGTGAAGGCTCCCAAGATCAGGC 1326
 Db 1236 CCTTGTGCTGCTCCCAAGAGCTTGCATGCGGCAACAAGTGAAGGCTCCCAAGATCAG- 1293
 QY 1327 CGCTTTTACGGGCTGATTTGTACGGTGGGCTCCACATGAGACTTCTGTGTCGGGCTT 1386
 Db 1294 CGCTTTTACGGGCTGATTTGTACGGTGGGCTCCACATGAGACTTCTGTGTCGGGCT- 1351
 QY 1387 GCCACAAAAGCTGTGAAGATGTCGAGTCTCTGGGTGCTCCAGACTGAGTTCTTTAGC 1446
 Db 1352 GCCACAAAAGCTGTGAAGATGTCGAGTCTCTGGGTGCTCCAGACTGAGTTCTTTA- 1409
 QY 1447 TTCAGAGATGGAGATTTCCCTACCAAGATTTGAGACAACAATATCCAGTATCCCAAC 1506
 Db 1410 TTCAGAGATGGAGATTTCCCTACCAAGATTTGAGACAACAATATCCAGTATCCCA- 1467
 QY 1507 TACTGTTCCTTCAAAAGCCAGAGTGTCTGATGAGAAACGCAATCGGAAGTGTCCGC 1566

Db 1468 TACTGTTCCTTCAAAAGCCAGAGTGTCTGATGAGAAACGCAATCGAAAGTGTCC--C 1525
 QY 1567 ATGAGATGCTGCAAGATGAGACTTACAGTCCGTGAGCCCTGGCAAAAGTGAAGAGT 1626
 Db 1526 ATGAGATGCTGCAAGATGAGACTTACAGTCCGTGAG--CCTGGCAAAAGTGAAGAGT 1584
 QY 1627 GTGCTGATGAGAGCCAGAGTTCAGACCTTGACTTAGGCCAGTTCCGATGAGCTGGC 1686
 Db 1585 G-CTTGTGATGAGAGCCAGAGTTCAGACCTTGACTTAGGCCAGTTCCGATGAGCTK- 1641
 QY 1687 GTCTATTTGCCCCACACCCAGCCCAACTGCCCCAGTTCTATTTGTTTGAAGACCCA 1746
 Db 1642 GTTATATTTGCCACACCCAGCCCAACTGCCCCAGTTCTATTTGTTTGAAGACCC-- 1699
 QY 1747 TTGCTTCAAGGCTGCCCTTCTGAGTCTGTTAATCCGGCCCTACTACATTTCTTGGGT 1806
 Db 1700 TTGCTTCAAGGCTGCCCTTCTGAGTCTGTTAATCCGGCCCTTAMTACATTTTCTTGG- 1757
 QY 1807 TGGAGCAACAGTCCACAGAGAGGCAAGGTGGAGCTGCGCCCTCTTAAAGATGACTT 1866
 Db 1758 TGGAGCAACAGTCCACAGAGAGGCAAGGTGGAGCTGCGCCCTCTTAAAGATGAC-- 1815
 QY 1867 TACATTAATATGTTGATCTTCAAAAAAAA 1895
 Db 1816 TACATTAATATGTTGATCTTCAAAAAAAA 1844

RESULT 11
 AAH9858
 ID AAH9858 standard; cDNA, 1671 BP.
 XX
 AC AAH9858;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein encoding cDNA sequence SEQ ID NO:693.
 XX
 KW Human, cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cyrostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200153455-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000MO-US035017.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dymnac RT;
 XX WPI, 2001-457603/49.
 DR P-PSDB; AAM25917.
 DR
 XX

CC AAH99166 to AAH99904 encode the human proteins given in AAM5225 to
CC CC
CC AAM5225. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; virocidic; anti-HIV; fungicide; antimitagen;
CC cardiovascular; anaemic; antigregant; haemostatic; vulnery;
CC anticancer; osteoporetic; dermatologic; antiallergic; antiaesthetic;
CC antidiabetic; cytotoxic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, infectious diseases, viral, bacterial, HIV and fungal
CC infections, autoimmune, genetic diseases, haemolytic disorders,
CC anaemia, platelet disorders, chromocytopenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders

Sequence 1671 BP; 361 A; 537 C; 432 G; 340 T; 28 U; 10 N; 1 S; 1 Y; 1 W; 1 X

Sequence 1671 BP; 361 A; 537 C; 424 G; 349 T; 0 U; 0 Other;

Query Match	67.1%	Score 1271.8;	DB 4;	Length 1671;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1273; Conservative	0;	Mismatches	0	

[illegible]

QY	691	GAGGGGCGAAGAACGGAAGCCAGAGAGAAACAGAAAGAGAGGAAAGCAGAGAA	750
Db	997	GAGGGGCGAAGAACGGAAGCCAGAGAGAAACAGAAAGAGAGGAAAGCAGAGAA	1056
QY	751	GGAAGAGGACCTAAGAGGAGCGGAGGCGTGTGTCTCAGCTGCACAGACTCAGAGCC	810
Db	1057	GGAAGAGGAGCTAAGAGGAGCGGAGGCGTGTGTCTCAGCTGCACAGACTCAGAGCC	1116
QY	811	AAGTTTCACTCTGAATCTCTATCTCTTAAACCTTCTCTTTTGTCTCCCGGGATCGAGAA	870
Db	1117	AAGTTTCACTCTGAATCTCTATCTCTTAAACCTTCTCTTTTGTCTCCCGGGATCGAGAA	1176
QY	871	GTAAGAGTCTACTCTTGAATGATGAAATGAGAAACATCCAGAGACTCATTCGATCAGCCACAGAA	930
Db	1177	GTAAGAGTCTACTCTTGAATGATGAAATGAGAAACATCCAGAGACTCATTCGATCAGCCACAGAA	1236
QY	931	ATAGATGAATGAATGAATGAATATATGATGAGAACTCTTACCTGAGAAACCAAAACCTTGGC	990
Db	1237	ATAGATGAATGAATGAATGAATATATGATGAGAACTCTTACCTGAGAAACCAAAACCTTGGC	1296
QY	991	AGCTTCTGCGACGTCGCGCCACACAGAGGCGCTTGTGCTGTGTGTGTGATTCGATCGTGTGAG	1050
Db	1297	AGCTTCTGCGACGTCGCGCCACACAGAGGCGCTTGTGCTGTGTGTGTGATTCGATCGTGTGAG	1356
QY	1051	AATTACCTGCATCATTAACCCCCACAGCCACAGGCGCTGGAAGTACATGAGAGAGAGATCTTT	1110
Db	1357	AATTACCTGCATCATTAACCCCCACAGGCGCCAGGCGCTGGAAGTACATGAGAGAGAGATCTTT	1416
QY	1111	GGTTTTCGGGAAGTCGATCTGTGAACAGCTTGTGGGCGGAGACATGTCTTACTGTGTCCCTC	1170
Db	1417	GGTTTTCGGGAAGTCGATCTGTGAACAGCTTGTGGGCGGAGACATGTCTTACTGTGTCCCTC	1476
QY	1171	TGTGACTTCTGCTCTTGAAAGCTGTGAGACAGTGTCACTAGAGGCGCAGCTGTGAGGGGCAA	1536
Db	1477	TGTGACTTCTGCTCTTGAAAGCTGTGAGACAGTGTCACTAGAGGCGCAGCTGTGAGGGGCAA	1596
QY	1231	CAATGTGCAACCTTCCCAACAAGATCTCCCTTGTGTCAAGCCCTTGTCTCTCCCAAGGCTTG	1290
Db	1537	CAATGTGCAACCTTCCCAACAAGATCTCCCTTGTGTCAAGCCCTTGTCTCTCCCAAGGCTTG	1596
QY	1291	TTCATTCGGCAACAGGATGAGGATCCCCAGAAATGAGGCGCTTTTACGGGCTGGAATTTGTAC	1350
Db	1597	TTCATTCGGCAACAGGATGAGGATCCCCAGAAATGAGGCGCTTTTACGGGCTGGAATTTGTAC	1656
QY	1351	GGTGGGCTCCACATG 1365	
Db	1657	GGTGGGCTCCACATG 1671	

RESULT 12	
AD0245654	
ID AD024565 standard; cDNA, 3306 BP.	
XX	
XX	
AC	AD024565;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Human PRO7347 encoding cDNA SEQ ID NO:204

KM	human; PEO; antihaemic; antiarthritic; antiinflammatory; antipsoriatic
KM	antirheumatic; dermatological; immunostimulant; immunosuppressive;
KM	osteoporotic; vasotropic; immune related disease;
KM	inflammatory immune response; rheumatoid arthritis; osteoarthritis;
KM	juvenile chronic arthritis; systemic lupus erythematosus;
KM	spondyloarthritis; idiopathic inflammatory scleritis;
KM	idiopathic inflammatory myopathy; Sjögren's syndrome;
KM	systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KM	autoimmune disease; immune-mediated skin disease; bullous skin disease;
KM	erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
KM	splenomegaly; leukopaenia; gene; ss.
XX	
OS	Homo sapiens.

Db 2216 GGTGGGCTCCACATGACTTCTGTGCCCCGGCTTCCACGAAAGGCTGTGAAGATGTC 2275
 QY 1411 CGAGTCTCTGGTGGCTCCAGACTGAGTCTTACCTTCCAGATGGGATTTCCCTACC 1470
 Db 2276 CGAGTCTCTGGTGGCTCCAGACTGAGTCTTACCTTCCAGATGGGATTTCCCTACC 2335
 QY 1471 AAGATTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAGCCAGAG 1530
 Db 2336 AAGATTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAAGCCAGAG 2395
 QY 1531 TGTCTGATGAGAAACCGCAATCGGAAGTGG 1560
 Db 2396 TGTCTGATGAGAAACCGCAATCGGAAGTGG 2425

RESULT 13

ADP19006
 ID ADP19006 standard; cDNA; 964 BP.

XX ADP19006;

DT 26-AUG-2004 (first entry)

DE Human secreted polynucleotide #262.

XX Human; secreted protein; gene; ss; genetic disease.

XX Homo sapiens.

PN US2004110939-A1.

XX 10-JUN-2004.

XX 15-OCT-2001; 2001US-00978360.

XX 17-DEC-1998; 98WO-IB002122.

XX 09-FEB-1999; 99WO-IB000282.

XX 21-JUN-2000; 2000WO-IB000951.

XX 15-SEP-2000; 2000US-00663600.

XX (GIST) GENSET SA.

XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;

XX Ductet A;

XX MPI; 2004-440404/41.

XX P-PSDB; ADP19411.

PS Claim 1; SEQ ID NO 262; 113bp; English.

The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polynucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

CC Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;

Query Match 49.5%; Score 937.6; DB 12; Length 964;
 Best Local Similarity 99.3%; Pred. No. 9,9e-237;
 Matches 948; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 30 GGGCGGATCTTCTCCGGCCATAGAGAACCGCTGGCTTCTTCCCTCACTCTGAA 89
 Db 2 GGGCGGATCTTCTCCGGCCATAGAGAACCGCTGGCTTCTTCCCTCACTCTGAA 61
 QY 90 GGTGCTCTCTGCTCTGCTGACCTGCGCAGCCAGATGAGATGAGCTCAGGCCCACTTC 149
 Db 62 GGTGCTCTCTGCTCTGCTGACCTGCGCAGCCAGATGAGATGAGCTCAGGCCCACTTC 121
 QY 150 AGGCAACCTCTCTCTCTCAACGAATACGAGCTTCTTGGCACTGCTGACTCAACCTG 209
 Db 122 AGGCAACCTCTCTCTCTCAACGAATACGAGCTTCTTGGCACTGCTGACTCAACCTG 181
 QY 210 GAAGCAGAGACTACCTGCGCTCCGCTGCAACCCAGCGCTCCGGAAATCCCACTGCT 269
 Db 182 GAAGCAGAGACTACCTGCGCTCCGCTGCAACCCAGCGCTCCGGAAATCCCACTGCT 241
 QY 270 CCAAGCTGACCAATATGAAACCAAGGCTTAGTGCCGATGAGTGTCTGCTCAACT 329
 Db 242 CCAAGCTGACCAATATGAAACCAAGGCTTAGTGCCGATGAGTGTCTGCTCAACT 301
 QY 330 CCTTATGCTCTCTGCTTGTGAGTCTTCTGCACTTCACTACTACCTGCTCAACT 389
 Db 302 CCTTATGCTCTCTGCTTGTGAGTCTTCTGCACTTCACTACTACCTGCTCAACT 361
 QY 390 CGTCTATATGCAAGAGAGTCTGTGTTCCAGCCAGTCTCTATCTCACTCACTCAAC 449
 Db 362 CGTCTATATGCAAGAGAGTCTGTGTTCCAGCCAGTCTCTATCTCTCTCACTCAAC 421
 QY 450 TCTCAAGGATATGAAAGCTTCAAGTGAAGTCAACCAACA -GATACCTTCCCACT 508
 Db 422 TCTCAAGGATATGAAAGCTTCAAGTGAAGTCAACCAACA -GATACCTTCCCACT 481
 QY 509 CACCCCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGAGAGGCTGACGA 568
 Db 482 CACCCCACTTCAAGTGAAGAGCCAGACCTTCCAGCCCTGAGAGGCTGACGA 541
 QY 569 ACAAGTGAAGAGCTCTTCAATCTCTTGTCCCTGAGAGCCAGAGCAAGCCAG 628
 Db 542 ACAAGTGAAGAGCTCTTCAATCTCTTGTCCCTGAGAGCCAGAGCAAGCCAG 601
 QY 629 AGCACAAGCAGAGCAGAGGTGAGACAGGAGAGCCGACACAAAGACAGAGG 688
 Db 602 AGCACAAGCAGAGCAGAGGTGAGACAGGAGAGCCGACACAAAGACAGAGG 661
 QY 689 AAGAGGCGCAGAAACAGAAAGAGCAGAAAGAGCAGAAAGAGAGGAGAGG 748
 Db 662 AAGAGGCGCAGAAACAGAAAGAGCAGAAAGAGCAGAAAGAGAGGAGAGG 721
 QY 749 AAGAGCAGGGGACATAGAGAGAGAGGAGGCTGTCTCAAGCTGCAAGACTCAAGC 808
 Db 722 AAGAGCAGGGGACATAGAGAGAGAGGAGGCTGTCTCAAGCTGCAAGACTCAAGC 781
 QY 809 CCAAGTTCACTCTGATCTCTATCTTCTTCAACCTTCTTGTGCTCCCGGATGAGG 868
 Db 782 CCAAGTTCACTCTGATCTCTATCTTCTTCAACCTTCTTGTGCTCCCGGATGAGG 841
 QY 869 AAGTAGGTCTACTCTCTATGATATGAGAACATCCAGAGAGCTCATTTGATGAGCCAGG 928
 Db 842 AAGTAGGTCTACTCTCTATGATATGAGAACATCCAGAGAGCTCATTTGATGAGCCAGG 901
 QY 929 AATATGATGAATGAATGAATATATGAGAGAACTCTCACTGAGAGAAACCAAA 983
 Db 902 AATATGATGAATGAATGAATATATGAGAGAACTCTCACTGAGAGAAACCAAA 956

RESULT 14

AA97739
 ID AA97739 standard; DNA; 964 BP.

XX

AA97739;
 13-SEP-1999 (first entry)
 Extended human secreted protein coding sequence, SEQ ID NO. 304.
 Secreted protein; human; cytokine; cellular proliferation; cell movement;
 cellular differentiation; immune system regulator; anti-inflammatory;
 haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
 reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 genetic disease; 88.
 Homo sapiens.
 MO991236-AZ.
 24-JUN-1999.
 17-DEC-1998; 98WO-1B002122.
 17-DEC-1997; 97US-0069957P.
 09-FEB-1998; 98US-0074121P.
 13-APR-1998; 98US-0081563P.
 10-AUG-1998; 98US-0096116P.
 (GEST) GENSET.
 Bougueleret L, Duclert A, Dumas Milne Edwards J;
 WPI; 1999-385906/32.
 P-PSDB; AAY36055.
 New isolated human secreted proteins.
 Claim 1; Page 377; 516pp; English.
 This sequence represents an extended human secreted protein coding
 sequence of the invention. The secreted proteins can be used in treating
 or controlling a variety of human conditions. The secreted proteins may
 act as cytokines or may affect cellular proliferation or differentiation
 or may act as immune system regulators, haematopoiesis regulators, tissue
 growth regulators, regulators of reproductive hormones or cell movement
 or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 tumour inhibition activity. The DNA can be used in forensic procedures
 to identify individuals or in diagnostic procedures to identify
 individuals having genetic diseases resulting from abnormal expression of
 the genes corresponding to the extended cDNAs. They are also useful for
 constructing a high resolution map of the human chromosomes. They can
 also be used for gene therapy to control or treat genetic diseases
 Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;
 Query Match 49.4%; Score 937; DB 2; Length 964;
 Best Local Similarity 99.3%; Pred. No. 1.4e-236;
 Matches 948; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 30 GGGCGATCTTCCGGCCATGAGAGCGAGCGCTTCTTCCCTCATCTCTGAA 89
 2 GGGCGATCTTCCGGCCATGAGAGCGAGCGCTTCTTCCCTCATCTCTGAA 61
 90 GGTGCTCTCTCTCTGACCTGCGAGCGAGCGAGATTGCACTGAGGCCCTCC 149
 62 GGTGCTCTCTCTCTGACCTGCGAGCGAGCGAGATTGCACTGAGGCCCTCC 121
 150 AGGCGATCTTCTCTCTGACCTGCGAGCGAGCGAGATTGCACTGAGGCCCT 209
 122 AGGCGATCTTCTCTCTGACCTGCGAGCGAGCGAGATTGCACTGAGGCCCT 181
 210 GAAGGAG 269
 182 GAAGGAG 241
 270 CGAGCTGAGCAATATGAAAAACAGCGCTTAGTGCCGATGTGCTCTCAACT 329

242 CCAGCTGAGCAATATGAAAAACAGCGCTTAGTGCCGATGTGCTCTCAACT 301
 330 CCCTTATGCTCTCTGATTTGAGCTTTTCCGAGTTCACTCACTGCTTCAACCA 389
 302 CCCTTATGCTCTCTGATTTGAGCTTTTCCGAGTTCACTCACTGCTTCAACCA 361
 390 CGTCTACTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 449
 362 CGTCTACTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
 450 TCTTCAAGAGATGAAAGCTTCACTGAGTTCACTCACTCACTCACTCACT 508
 422 TCTCAAGAGATGAAAGCTTCACTGAGTTCACTCACTCACTCACTCACT 481
 509 CACCCCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568
 482 CACCCCACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
 569 ACAAGCTGAG 628
 542 ACAAGCTGAG 601
 629 AGCACAAG 668
 602 AGCACAAG 661
 689 AAG 748
 662 AAG 721
 749 AAG 808
 722 AAG 781
 809 CCAAGTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
 782 CCAAGTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
 869 AAGTAAAGTACTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 928
 842 AAGTAAAGTACTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901
 929 AAGTAAAGTACTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
 902 AAGTAAAGTACTCTTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 956
 RESULT 15
 AD053839
 ID AD053839 standard; DNA; 695 BP.
 AC AD053839;
 XX 21-OCT-2004 (first entry)
 DE Novel canine microarray-related DNA sequence SeqID5141.
 XX canine microarray; drug screening; toxicity assay;
 XX environmental pollutant; cellular response; gene expression profile;
 XX toxic response; liver necrosis; fatty liver disease;
 XX protein adduct formation; hepatitis; dog; ds.
 OS Canis familiaris.
 XX
 PN WO2004063324-A2.
 XX 29-JUL-2004.
 PD
 XX 05-MAY-2003; 2003WO-US013853.
 XX 03-MAY-2002; 2002US-0377240P.
 XX

PA (GENE-) GENE LOGIC INC.
 PA (PFIZ) PFIZER PROD INC.

XX Digians JC, Porter M, Wei T;
 XX

DR WPI; 2004-561890/54.

PT New isolated nucleic acid molecule, useful for drug screening and
 PT toxicity assays or for assessing the impact, including toxicity, of a
 PT compound, pharmaceutical agent or environmental pollutant on a cell or
 PT living organism.

PS Claim 1; SEQ ID NO 5141; 41bp; English.

CC This invention is related to a novel isolated canine nucleic acid
 CC sequences and the construction of canine microarrays containing a
 CC significant portion of the canine genome. The isolated canine nucleic
 CC acid sequences of the invention may be useful for drug screening and
 CC toxicity assays. The invention is therefore useful for assessing the
 CC impact, including toxicity, of a compound, pharmaceutical agent or
 CC environmental pollutant on a cell or living organism. The methods are
 CC useful for detecting genes that are up- or down-regulated in canines in a
 CC disease state. The sequences are useful as diagnostic agents or markers
 CC to detect a cellular response in a sample individually or as part of a
 CC gene expression profile. It is also useful as a target for agents that
 CC modulate gene expression or activity. The database is useful for
 CC producing electronic Northern blots that allow the user to determine the cell
 CC type or tissue in which a given gene is expressed and to allow
 CC determination of the abundance or expression level of a given gene in a
 CC particular tissue or cell. The methods are useful for determining the
 CC similarity of a toxic response to one or more individual compounds. The
 CC methods are useful for predicting at least one toxic response or the
 CC likelihood that a compound or test agent will induce various specific
 CC pathologies such as those of the liver (liver necrosis, fatty liver
 CC disease, protein adduct formation or hepatitis), those of the kidney,
 CC heart, brain or testes, or other pathologies associated with at least one
 CC of the toxins. The methods are also useful for predicting or elucidating
 CC the potential cellular pathways influenced, induced or modulated by the
 CC compound or test agent due to the similarity of the expression profile
 CC compared to the profile induced by a known toxin. The present sequence is
 CC that of a canine DNA sequence which was claimed for use during the
 CC production of a canine microarray of the invention.

XX Sequence 695 BP; 157 A; 209 C; 169 G; 159 T; 0 U; 1 Other;

Query Match

Best Local Similarity 25.3%; Score 479.2; DB 13; Length 695;

Matches 575; Conservative 0; Mismatches 109; Indels 11; Gaps 2;

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QY 1177 TTCTGCTCTTGAAGCTGAGAGCTGCACTCAGAGGCGCAAGCTGAGCGGCAACAATGC 1236
Db 1 TTCTGCTCTTGAAGCTGAGAGCTGCACTCAGAGGCGCAATCMTGCAAGCGGCAAGCTGTGT 60
QY 1237 GACACCTTCCACAGAGCTCCCTTGTGAGCCCTTGTGCTTCCCTCCAGAGCTGTCCATC 1296
Db 61 GACAGCTTCCACAAACACCTTGTGAGCCCTTGTGCTTCCCTCCAGAGCTGTCCATC 120
QY 1297 GGCACCAAGAGTGGGCTCCCAAGATCAGGCGGCTTTTACGCGGTGATTTGTAAGGTGGG 1356
Db 121 GGTACCCAGGTAGGAAACCCCAACATCAGCGGCTTCTACGGGCTGATATGTATGGCGGA 180
QY 1357 CTCACATGAGACTTCTGAGTGGCGGCTTGCACAGAAAGCTGTGAGATGTCCGAGTC 1416
Db 181 CTCGCAATGAGACTTCTGAGTGGCGGCTTGCACAGAAAGCTGTGAGATGTCCGAGTC 240
QY 1417 TCTGGGTGGCTCCAGACTGAGTCTTAGCTTCCAGATGGGGAATTCCTTCAAGATTT 1476
Db 241 TCCGGCTGGCTCCAGAGAAATTCCTTAGCTTCCAGATGGGGAATTTCCCAACAAGATT 300
QY 1477 TGTGACACAGACTATATCCAGTACCAAACTACTGTTCTTCAAAAGCCAGAGAGTGTCTG 1536
Db 301 TGTGACACAGACTATATGATGATCCAAACTACTGTGCTTCAAAAGCCAAAGAGTGTCTG 360

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QY 1537 ATGAAACCGCANTGGAGAGTGTCCCGCATGAGATGTCTGCAGATAGACTTACAT 1596
Db 361 ATGAAACCGCGAGACCGGAAAGTGTCCCGCATGAGATGTCTGCAGATAGACTTACAT 420
QY 1597 GCCTGAGCCCTGCAAAAGTGAAGACGTTGTGCTTCGATGAGCCAGAGTTCAGACAC 1656
Db 421 GTCTTAAGCCAGGCAAAACGAGAGACCTTGTACTTCGATGAGCCAGAAATTCAGACAC 480
QY 1657 TTGACTAGGCGCAGTTGCAATGAGTGGCGCTGTATTTGCCCCAACCCAGCCCAACT 1716
Db 481 TTGACTTAGGCGCAAGGTGATGAACTGAGTTCAGTTCACCTCCACCCAGCCCAACT 540
QY 1717 GCCCAGTCTCTATTTGTTTGAAGCCCA-----TTGCTTCAAGGCTGCCCCCTT 1766
Db 541 TCCCACTTCTCATTGCTTGAAGCCCATGTGTCAGTTTCTTCTTGGCTGCACTT 600
QY 1767 CTGGTCTGTACTGCGGCCCTCACTCAATTT-CTTGGGTTGAGCAACAGTCCAGAG 1825
Db 601 GTGGGTCTTCACCTTGGCCCTGACTCAATTTGCTGGGTTGAGCAAGTCCAGAG 660
QY 1826 AGGCGCACGATGGAGCTGCGCCCTCTCTTAAGA 1860
Db 661 AGGTCCATGATGGGCACTCCACTTGAAGA 695

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Search completed: March 7, 2005, 15:17:14
 Job time : 1062 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 17:40:21 ; Search time 1053 Seconds
(without alignments)
10653.286 Million cell updates/sec

Title: US-09-559-013E-23

Sequence: 1 gtagagcgcgtctgtctc.....tgtagcttcaaaaaaaaa 1895

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: geneseqn1800s:*
2: geneseqn1390s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1895	100.0	1895	5	AAD08658 Human can
2	1886	99.5	1886	6	ABT14679 Human can
3	1742	91.9	1912	3	AAZ50927 Human Pro
4	1494	78.8	1889	2	AAZ06785 Human adu
5	1284	67.8	1882	2	AAZ24890 Human sec
6	1284	67.8	1892	8	ADA39940 Human sec
7	1284	67.8	1892	10	ADC73578 Human sec
8	1284	67.8	1892	10	ADD37623 Human sec
9	1284	67.8	1892	10	ADA56130 Gene enco
10	1173	61.9	1671	4	AAH99858 Human pro
11	536	28.3	3306	12	AD024565 Human pro
12	528	27.9	964	2	AAH97739 Extended
13	528	27.9	964	12	ADP19006 Human sec
14	379	20.0	469	9	ACH27630 Human adu
15	339	17.9	516	8	ABZ72003 Human ful
16	307	16.2	474	9	ACH49259 Human leu
17	281	14.8	308	2	AAV68163 ESR clone
18	280	14.8	507	8	ABZ71923 Human can
19	280	14.8	522	8	ABZ71705 Human can
20	199	10.5	199	8	ABZ19225 Group III

21	116	6.1	1854	9	ADA45034	Ada45034 Human pol
22	112	5.9	128	2	AAZ51481	Aax51481 Human sec
23	63	3.3	387	8	ABZ19899	Abz19899 Group III
24	60	3.2	60	6	ABNA9513	Abna9513 Human spl
25	31	1.6	695	13	AD053839	Adg53839 Novel can
26	27	1.4	29	2	AAZ06795	Aax06795 Human sec
27	27	1.4	29	9	ADA45049	Ada45049 Human o11
28	23	1.2	23	5	AAD08668	Aad08668 Human OY
29	23	1.2	345	6	ABZ51553	Abz51553 Human CDN
30	22	1.2	22	5	AAD08665	Aad08665 Human tes
31	21	1.1	21	10	AAD08664	Aad08664 Human tes
32	21	1.1	450	10	ADP80420	Adf80420 Leukemia
33	21	1.1	249	3	AAZ76271	Aac76271 Human ORF
34	21	1.1	2684	13	ACNA40762	Actn40762 Tumour-as
35	21	1.1	28564	10	ADZ63335	Adz63335 Human gen
36	21	1.1	59767	13	ABD32905	Abd32905 Mouse can
37	20	1.1	20	5	AAD08663	Aad08663 Human OY
38	20	1.1	20	5	AAD08662	Aad08662 ht-3 RT-P
39	20	1.1	20	5	AAD08661	Aad08661 ht-5 RT-P
40	20	1.1	20	5	AAD08666	Aad08666 Human tes
41	20	1.1	20	8	ABT14666	Abt14666 Human can
42	20	1.1	20	8	ABT14665	Abt14665 Human can
43	20	1.1	466	4	AAK33554	Aak33554 Human bon
44	20	1.1	466	4	ABS33337	Abs33337 Human liv
45	20	1.1	466	6	ABS08423	Abs08423 Human gen
46	20	1.1	738	12	ADQ27055	Adq27055 Human ant
47	20	1.1	792	11	ABD01111	Abd01111 Klebsiell
48	20	1.1	1364	6	ABN98242	Abn98242 Arabidops
49	20	1.1	1701	11	ABD01223	Abd01223 Klebsiell
50	20	1.1	3094	4	ABL27444	Ab127444 Drosophill
51	20	1.1	3471	10	ADA53602	Ada53602 Human cod
52	20	1.1	5235	12	ADM31027	Adm31027 Human cal
53	20	1.1	6232	2	AAQ29269	Aaq29269 Human cal
54	20	1.1	6792	12	ADM31025	Adm31025 Human cal
55	20	1.1	7175	2	AAQ37818	Aaq37818 Sequence
56	20	1.1	7175	2	AAQ84658	Aaq84658 Human neu
57	20	1.1	7175	2	AAV42686	Aav42686 DNA encod
58	20	1.1	7175	3	AAV71704	Aav71704 Human cal
59	20	1.1	7175	6	AAZ39956	Aaz39956 Human cal
60	20	1.1	7175	12	ADJ38318	Adj38318 Human cal
61	20	1.1	7175	12	ADM57706	Adm57706 Human cal
62	20	1.1	7177	8	ABZ58367	Abz58367 Human N-t
63	20	1.1	7266	2	AAV29059	Aav29059 Human cal
64	20	1.1	7362	2	AAQ37817	Aaq37817 Sequence
65	20	1.1	7362	2	AAQ84657	Aaq84657 Human neu
66	20	1.1	7362	2	AAV42685	Aav42685 DNA encod
67	20	1.1	7362	3	AAV71703	Aav71703 Human cal
68	20	1.1	7362	6	AAZ39955	Aaz39955 Human cal
69	20	1.1	7362	12	ADJ38316	Adj38316 Human cal
70	20	1.1	7362	12	ADM57705	Adm57705 Human cal
71	20	1.1	7363	12	ADQ22372	Adq22372 Human sof
72	20	1.1	7364	6	ABL65869	Ab165869 Lung canc
73	20	1.1	7364	8	ABZ58366	Abz58366 Human N-t
74	20	1.1	7364	12	ADP21335	Adp21335 Gene CACN
75	20	1.1	7364	13	ADZ43909	Adz43909 Human N-t
76	20	1.1	7376	2	AAZ88001	Aax88001 N-type ca
77	20	1.1	7376	13	ADR43931	Adr43931 N-type ca
78	20	1.1	26214	12	ADQ97246	Adq97246 Mouse can
79	20	1.1	72352	12	ADQ97067	Adq97067 Mouse can
80	20	1.1	77834	11	ACNA4076	Actn4076 Mouse gen
81	20	1.1	110000	10	ACFA24745	Actf24745 Mouse gen
82	20	1.1	198073	11	ACNA4302	Actn4302 Human gen
83	19	1.0	19	5	AAD08667	Aad08667 Human OY
84	19	1.0	252	10	ACF69362	Actf69362 Phototrab
85	19	1.0	307	12	ADH00168	Adh00168 Bovine ES
86	19	1.0	334	8	ABX37455	Abx37455 Bovine ES
87	19	1.0	367	3	AAZ27942	Aaz27942 Human sec
88	19	1.0	378	6	ABN22892	Abn22892 Human ORF
89	19	1.0	440	8	ABX65257	Abx65257 Human gen
90	19	1.0	603	3	AAZ80160	Aaz80160 Human col
91	19	1.0	711	12	ADQ35812	Adq35812 Novel mou
92	19	1.0	963	5	AAZ63215	Aaz63215 Human pur
93	19	1.0	1069	5	AAZ87758	Aaz87758 DNA encod

94	19	1.0	1069	5	AA878277	AA878277 DNA encod	C 167	18	0.9	100	8	ACD72083	AcD72083 E. coli K
95	19	1.0	1112	3	AA876384	AA876384 Human ORF	C 168	18	0.9	100	8	ACD78582	AcD78582 E. coli K
96	19	1.0	1287	3	AA89404	AA89404 Beta-prim	C 169	18	0.9	100	8	ACD78583	AcD78583 E. coli K
97	19	1.0	1521	3	AA89407	AA89407 Open read	C 170	18	0.9	155	3	ADF57263	AdF57263 Urogenita
98	19	1.0	1595	13	ACN38532	ACN38532 Tumour	C 171	18	0.9	157	3	ACB13527	ACB13527 Human sec
99	19	1.0	1665	8	ACN44709	ACN44709 Prokaryot	C 172	18	0.9	175	5	ABA12653	ABA12653 Human sec
100	19	1.0	1713	10	ADFO0423	ADFO0423 Bacterial	C 173	18	0.9	191	3	ACB16726	ACB16726 Human sec
101	19	1.0	1834	5	ACA39756	ACA39756 Prokaryot	C 174	18	0.9	201	13	ADS38781	ADS38781 Human sec
102	19	1.0	1834	5	AA868454	AA868454 DNA encod	C 175	18	0.9	227	6	ABK39586	ABK39586 Human aut
103	19	1.0	2000	6	ABZ15642	ABZ15642 Arabidops	C 176	18	0.9	227	8	ACA11932	ACA11932 Human lun
104	19	1.0	2139	8	ACA20568	ACA20568 Prokaryot	C 177	18	0.9	227	8	ACA11932	ACA11932 Human lun
105	19	1.0	2201	13	ACN39007	ACN39007 Tumour-as	C 178	18	0.9	227	8	ACA03118	ACA03118 Lung can
106	19	1.0	2201	13	ACN39383	ACN39383 Tumour-as	C 179	18	0.9	227	8	ACA03118	ACA03118 Lung can
107	19	1.0	2236	4	AB109505	AB109505 Drosophi	C 180	18	0.9	227	8	ACA03118	ACA03118 Lung can
108	19	1.0	2570	4	AA809393	AA809393 Drosophi	C 181	18	0.9	227	8	ACA03118	ACA03118 Lung can
109	19	1.0	2597	4	AA866902	AA866902 Human EXM	C 182	18	0.9	227	10	ADH47143	ADH47143 Human lun
110	19	1.0	2652	5	AA885132	AA885132 DNA encod	C 183	18	0.9	227	10	ADH47143	ADH47143 Human lun
111	19	1.0	2652	10	ADBE09933	ADBE09933 Novel DNA	C 184	18	0.9	227	13	ADJ21079	ADJ21079 Human lun
112	19	1.0	2665	4	AAH16002	AAH16002 Human cDN	C 185	18	0.9	227	13	ADJ21062	ADJ21062 Human lun
113	19	1.0	2671	2	AAZ03648	AAZ03648 Ras p21	C 186	18	0.9	244	4	ABK75085	ABK75085 Human bra
114	19	1.0	2671	2	AAZ03648	AAZ03648 Human RGT	C 187	18	0.9	244	4	ABK75085	ABK75085 Human bra
115	19	1.0	3076	4	AAH18516	AAH18516 Human CDN	C 188	18	0.9	244	4	ABK75085	ABK75085 Human bra
116	19	1.0	3080	4	AA891322	AA891322 Human PDI	C 189	18	0.9	244	4	ABK75085	ABK75085 Human bra
117	19	1.0	3975	4	AAK94374	AAK94374 Human PDI	C 190	18	0.9	244	4	ABK75085	ABK75085 Human bra
118	19	1.0	3975	12	ADL31072	ADL31072 Full leng	C 191	18	0.9	244	4	ABK75085	ABK75085 Human bra
119	19	1.0	4028	5	ADM19259	ADM19259 Novel hum	C 192	18	0.9	244	4	ABK75085	ABK75085 Human bra
120	19	1.0	4069	6	ABN59810	ABN59810 Novel hum	C 193	18	0.9	244	4	ABK75085	ABK75085 Human bra
121	19	1.0	4088	5	ADL62737	ADL62737 Human ova	C 194	18	0.9	329	3	AA856980	AA856980 Plasm rad
122	19	1.0	4383	4	AB109783	AB109783 Drosophi	C 195	18	0.9	348	3	AA857020	AA857020 Human sec
123	19	1.0	4408	10	ADG28471	ADG28471 Rubella v	C 196	18	0.9	388	10	ACD95643	ACD95643 Human col
124	19	1.0	5076	5	AA868170	AA868170 DNA encod	C 197	18	0.9	388	10	ACD95643	ACD95643 Human col
125	19	1.0	5076	5	AA882123	AA882123 DNA encod	C 198	18	0.9	448	5	AA878825	AA878825 DNA encod
126	19	1.0	5076	5	AA872828	AA872828 DNA encod	C 199	18	0.9	454	5	AA878825	AA878825 DNA encod
127	19	1.0	5076	5	AA870245	AA870245 DNA encod	C 200	18	0.9	461	11	ADT94743	ADT94743 Human col
128	19	1.0	5076	5	AA874989	AA874989 DNA encod	C 201	18	0.9	463	9	ACH45506	ACH45506 Human foe
129	19	1.0	5178	6	AA878732	AA878732 DNA encod	C 202	18	0.9	471	13	ADG95013	ADG95013 Human the
130	19	1.0	6056	6	AB133027	AB133027 DNA imm	C 203	18	0.9	472	8	ABZ26648	ABZ26648 Human GEN
131	19	1.0	6160	12	ADJ12530	ADJ12530 DNA fragm	C 204	18	0.9	474	5	AA876690	AA876690 DNA encod
132	19	1.0	6279	4	AB109392	AB109392 Drosophi	C 205	18	0.9	474	5	AA876690	AA876690 DNA encod
133	19	1.0	6480	10	ABZ67665	ABZ67665 Human sec	C 206	18	0.9	474	5	AA876690	AA876690 DNA encod
134	19	1.0	9120	4	AB109782	AB109782 Drosophi	C 207	18	0.9	496	5	AA877936	AA877936 DNA encod
135	19	1.0	9588	10	ADG37082	ADG37082 Vector pP	C 208	18	0.9	502	12	ACH73203	ACH73203 Human gen
136	19	1.0	9661	2	AA809504	AA809504 Drosophi	C 209	18	0.9	502	12	ACH73203	ACH73203 Human gen
137	19	1.0	9757	2	AA809768	AA809768 Infection	C 210	18	0.9	504	12	ADN98624	ADN98624 Novel hum
138	19	1.0	9759	3	AA808943	AA808943 Rubella v	C 211	18	0.9	504	12	ADN98624	ADN98624 Novel hum
139	19	1.0	9759	10	ADG28462	ADG28462 Rubella v	C 212	18	0.9	514	12	ACH73601	ACH73601 Human gen
140	19	1.0	9759	10	ADG28462	ADG28462 Rubella v	C 213	18	0.9	518	5	AA866352	AA866352 Human gen
141	19	1.0	9759	10	ADG28462	ADG28462 Rubella v	C 214	18	0.9	520	10	ADBE6411	ADBE6411 Human gen
142	19	1.0	9762	3	AAZ48249	AAZ48249 Rubella v	C 215	18	0.9	522	5	AA871834	AA871834 DNA encod
143	19	1.0	10450	5	AA871127	AA871127 DNA encod	C 216	18	0.9	528	10	ABX57531	ABX57531 Arabidops
144	19	1.0	10992	4	AAK69375	AAK69375 Human imm	C 217	18	0.9	535	5	AA875559	AA875559 DNA encod
145	19	1.0	28198	10	ADG37080	ADG37080 Mouse pla	C 218	18	0.9	547	5	AA878851	AA878851 DNA encod
146	19	1.0	36241	10	ADH74385	ADH74385 Mycobacte	C 219	18	0.9	550	6	ABD31375	ABD31375 Amplicon
147	19	1.0	47613	11	ACN44072	ACN44072 Mouse gen	C 220	18	0.9	588	12	ACH69097	ACH69097 Human gen
148	19	1.0	59458	13	ADH67037	ADH67037 Murine ca	C 221	18	0.9	597	4	AAI17628	AAI17628 Probe #75
149	19	1.0	59458	13	ADH67037	ADH67037 Murine can	C 222	18	0.9	597	4	AAI17628	AAI17628 Probe #75
150	19	1.0	63588	8	ABSS7150	ABSS7150 Human gen	C 223	18	0.9	597	4	AAI17628	AAI17628 Probe #75
151	19	1.0	72705	11	ACN45158	ACN45158 Human gen	C 224	18	0.9	597	4	AAI17628	AAI17628 Probe #75
152	19	1.0	100267	6	ABT11032	ABT11032 Human bre	C 225	18	0.9	597	4	AAI17628	AAI17628 Probe #75
153	19	1.0	100779	12	ACF65386	ACF65386 Mouse can	C 226	18	0.9	597	4	AAI17628	AAI17628 Probe #75
154	19	1.0	103471	12	ADG97668	ADG97668 Mouse can	C 227	18	0.9	597	4	AAI17628	AAI17628 Probe #75
155	19	1.0	110000	4	AAK95240	AAK95240 of	C 228	18	0.9	597	4	AAI17628	AAI17628 Probe #75
156	19	1.0	110000	6	ABT00010	ABT00010 of	C 229	18	0.9	597	4	AAI17628	AAI17628 Probe #75
157	19	1.0	110000	6	ABT00010	ABT00010 of	C 230	18	0.9	597	4	AAI17628	AAI17628 Probe #75
158	19	1.0	110000	6	ABT00010	ABT00010 of	C 231	18	0.9	597	4	AAI17628	AAI17628 Probe #75
159	19	1.0	110000	6	ABT00010	ABT00010 of	C 232	18	0.9	597	4	AAI17628	AAI17628 Probe #75
160	19	1.0	110000	12	ADH74486	ADH74486 of	C 233	18	0.9	597	4	AAI17628	AAI17628 Probe #75
161	19	1.0	110000	12	ADH74486	ADH74486 of	C 234	18	0.9	597	4	AAI17628	AAI17628 Probe #75
162	19	1.0	348101	13	ABD31143	ABD31143 Murine ca	C 235	18	0.9	622	5	AA878280	AA878280 DNA encod
163	19	1.0	348101	13	ADQ97146	ADQ97146 Human can	C 236	18	0.9	639	5	AA878280	AA878280 DNA encod
164	19	0.9	20	6	AA893267	AA893267 Human STR	C 237	18	0.9	648	6	ABT11316	ABT11316 Yeast sel
165	19	0.9	29	10	AC893209	AC893209 Human STR	C 238	18	0.9	657	12	ADM91175	ADM91175 Human DNA
166	19	0.9	91	3	AA813481	AA813481 Human sec	C 239	18	0.9	663	5	ABV21703	ABV21703 Human pro

C 240	18	0.9	663	5	ABV27525	Abv27525 Human pto	C 313	18	0.9	1098	10	ADF57967	Adf57967 Human pol
C 241	18	0.9	667	13	ADQ55795	Adq55795 Novel can	C 314	18	0.9	1104	5	AA581509	AA581509 Pseudom
C 242	18	0.9	669	12	ADP29132	Adp29132 Human sec	C 315	18	0.9	1113	11	ABD05544	ABD05544 Pseudom
C 243	18	0.9	679	6	ABT11384	Abt11384 Yeast bel	C 316	18	0.9	1116	5	AA585777	AA585777 DNA encod
C 244	18	0.9	680	6	ABS62810	Abs62810 Selected	C 317	18	0.9	1120	5	AA579628	AA579628 DNA encod
C 245	18	0.9	681	12	AD000355	Ad000355 Novel hum	C 318	18	0.9	1122	5	AA585423	AA585423 DNA encod
C 246	18	0.9	693	12	ADN98796	Adn98796 Novel hum	C 319	18	0.9	1136	6	ABX97158	Abx97158 Human CNV
C 247	18	0.9	694	10	ACD93582	Acd93582 Human col	C 320	18	0.9	1136	12	ADN62032	Adn62032 Human ova
C 248	18	0.9	694	10	ACD93582	Acd93582 Human col	C 321	18	0.9	1155	5	AA572857	AA572857 DNA encod
C 249	18	0.9	732	5	AA567701	AA567701 DNA encod	C 322	18	0.9	1158	5	AA587752	AA587752 DNA encod
C 250	18	0.9	743	5	AA577336	AA577336 DNA encod	C 323	18	0.9	1162	5	AA570325	AA570325 DNA encod
C 251	18	0.9	749	6	ABT11524	Abt11524 Yeast bel	C 324	18	0.9	1167	5	AA566291	AA566291 DNA encod
C 252	18	0.9	750	6	ABS62919	Abs62919 Selected	C 325	18	0.9	1179	5	AA587847	AA587847 DNA encod
C 253	18	0.9	754	5	AAH64911	AAH64911 Human sec	C 326	18	0.9	1188	5	AA589552	AA589552 DNA encod
C 254	18	0.9	756	5	AA591722	AA591722 DNA encod	C 327	18	0.9	1189	5	AA587858	AA587858 DNA encod
C 255	18	0.9	756	5	AA587828	AA587828 DNA encod	C 328	18	0.9	1194	5	AA568938	AA568938 DNA encod
C 256	18	0.9	756	5	AA566348	AA566348 DNA encod	C 329	18	0.9	1206	5	AA566357	AA566357 DNA encod
C 257	18	0.9	798	12	AD000447	Ad000447 Novel hum	C 330	18	0.9	1206	5	AA570917	AA570917 DNA encod
C 258	18	0.9	798	12	ADN98878	Adn98878 Novel hum	C 331	18	0.9	1206	5	AA578262	AA578262 DNA encod
C 259	18	0.9	809	5	AA574396	AA574396 DNA encod	C 332	18	0.9	1206	5	AA577459	AA577459 DNA encod
C 260	18	0.9	809	5	AA572025	AA572025 DNA encod	C 333	18	0.9	1206	5	AA577459	AA577459 DNA encod
C 261	18	0.9	826	5	AA571059	AA571059 DNA encod	C 334	18	0.9	1206	10	ADG43735	Adg43735 Human N-a
C 262	18	0.9	833	8	AA515961	AA515961 Human ext	C 335	18	0.9	1223	5	AA571242	AA571242 DNA encod
C 263	18	0.9	834	5	AA587839	AA587839 DNA encod	C 336	18	0.9	1224	5	AA566364	AA566364 DNA encod
C 264	18	0.9	848	10	ADG43737	Adg43737 Human N-a	C 337	18	0.9	1224	5	AA587833	AA587833 DNA encod
C 265	18	0.9	849	10	ADG43732	Adg43732 Human N-a	C 338	18	0.9	1230	5	AA587757	AA587757 DNA encod
C 266	18	0.9	858	5	AA566367	AA566367 DNA encod	C 339	18	0.9	1230	5	AA574408	AA574408 DNA encod
C 267	18	0.9	865	5	AA591659	AA591659 DNA encod	C 340	18	0.9	1230	5	AA579617	AA579617 DNA encod
C 268	18	0.9	870	5	AA569934	AA569934 DNA encod	C 341	18	0.9	1231	5	AA586648	AA586648 DNA encod
C 269	18	0.9	891	5	AA581228	AA581228 DNA encod	C 342	18	0.9	1231	6	ABT07104	Abt07104 Human ova
C 270	18	0.9	895	5	AA570927	AA570927 DNA encod	C 343	18	0.9	1238	8	ABX72982	Abx72982 Human ova
C 271	18	0.9	895	5	AA587853	AA587853 DNA encod	C 344	18	0.9	1253	5	AA579833	AA579833 DNA encod
C 272	18	0.9	895	5	AA577942	AA577942 DNA encod	C 345	18	0.9	1253	5	AA579333	AA579333 DNA encod
C 273	18	0.9	900	5	AA588428	AA588428 DNA encod	C 346	18	0.9	1253	12	ADJ40269	Adj40269 Plant cDN
C 274	18	0.9	930	12	ADN98799	Adn98799 Novel hum	C 347	18	0.9	1266	5	AA585569	AA585569 DNA encod
C 275	18	0.9	930	12	AD000368	Ad000368 Novel hum	C 348	18	0.9	1266	5	AA579624	AA579624 DNA encod
C 276	18	0.9	936	3	AA571939	AA571939 Aspergill	C 349	18	0.9	1266	5	AA577084	AA577084 DNA encod
C 277	18	0.9	936	12	ADP29131	Adp29131 Human sec	C 350	18	0.9	1281	5	AA577933	AA577933 DNA encod
C 278	18	0.9	939	5	AA566384	AA566384 DNA encod	C 351	18	0.9	1281	5	AA576684	AA576684 DNA encod
C 279	18	0.9	942	5	AA571060	AA571060 DNA encod	C 352	18	0.9	1287	5	AA571110	AA571110 DNA encod
C 280	18	0.9	948	5	AA566350	AA566350 DNA encod	C 353	18	0.9	1287	5	AA573976	AA573976 DNA encod
C 281	18	0.9	951	3	AA547433	AA547433 Sequence	C 354	18	0.9	1290	5	AA591670	AA591670 DNA encod
C 282	18	0.9	951	12	ADL12382	Adl12382 Human ste	C 355	18	0.9	1296	5	AA570688	AA570688 DNA encod
C 283	18	0.9	960	2	AA566233	AA566233 Human HAP	C 356	18	0.9	1296	5	AA570926	AA570926 DNA encod
C 284	18	0.9	975	5	AA585563	AA585563 DNA encod	C 357	18	0.9	1302	11	ABD05854	ABD05854 Pseudom
C 285	18	0.9	981	10	ADG12659	Adg12659 Human GPC	C 358	18	0.9	1303	5	AA570697	AA570697 DNA encod
C 286	18	0.9	981	10	ADG43734	Adg43734 Human N-a	C 359	18	0.9	1308	10	ACF70488	Actf70488 Phototrab
C 287	18	0.9	983	3	AA59716	AA59716 Human sec	C 360	18	0.9	1311	5	AA566372	AA566372 DNA encod
C 288	18	0.9	987	10	ADG43738	Adg43738 Human N-a	C 361	18	0.9	1314	10	AA599606	AA599606 MDDT re1a
C 289	18	0.9	1000	6	ABN96965	Abn96965 Gene #346	C 362	18	0.9	1314	11	ABD05686	ABD05686 Pseudom
C 290	18	0.9	1000	13	ADR83512	Adr83512 Human pol	C 363	18	0.9	1314	13	ADP48908	Adp48908 Bacterial
C 291	18	0.9	1012	6	AB551033	Ab551033 Human cDN	C 364	18	0.9	1323	5	AA577935	AA577935 DNA encod
C 292	18	0.9	1014	8	ACA51828	Aca51828 Prokaryot	C 365	18	0.9	1326	5	AA566286	AA566286 DNA encod
C 293	18	0.9	1017	12	ADN98784	Adn98784 Novel hum	C 366	18	0.9	1341	5	AA588755	AA588755 DNA encod
C 294	18	0.9	1017	12	AD000353	Ad000353 Novel hum	C 367	18	0.9	1341	5	AA569190	AA569190 DNA encod
C 295	18	0.9	1017	12	ADP28802	Adp28802 Human sec	C 368	18	0.9	1341	5	AA577938	AA577938 DNA encod
C 296	18	0.9	1024	10	AB578366	Ab578366 Toxiciolog	C 369	18	0.9	1347	5	AA584798	AA584798 DNA encod
C 297	18	0.9	1027	5	AA577087	AA577087 DNA encod	C 370	18	0.9	1356	5	AA584781	AA584781 DNA encod
C 298	18	0.9	1032	5	AA575883	AA575883 DNA encod	C 371	18	0.9	1356	5	AA579835	AA579835 DNA encod
C 299	18	0.9	1035	5	AA569354	AA569354 DNA encod	C 372	18	0.9	1356	5	AA566356	AA566356 DNA encod
C 300	18	0.9	1035	5	AA588160	AA588160 DNA encod	C 373	18	0.9	1356	5	AA579330	AA579330 DNA encod
C 301	18	0.9	1035	5	AA579632	AA579632 DNA encod	C 374	18	0.9	1356	5	AA592240	AA592240 DNA encod
C 302	18	0.9	1041	5	AA566287	AA566287 DNA encod	C 375	18	0.9	1356	5	AA566285	AA566285 DNA encod
C 303	18	0.9	1050	8	ACA19022	Aca19022 Prokaryot	C 376	18	0.9	1359	5	AA584438	AA584438 DNA encod
C 304	18	0.9	1050	13	AD546033	Ad546033 Bacterial	C 377	18	0.9	1359	10	ADP59865	Adp59865 Human cDN
C 305	18	0.9	1052	4	ABK42676	Abk42676 Genomic B	C 378	18	0.9	1360	6	AA555225	AA555225 Human TRN
C 306	18	0.9	1052	5	ADB60832	Adb60832 Connectiv	C 379	18	0.9	1374	5	AA566369	AA566369 DNA encod
C 307	18	0.9	1056	5	AA571111	AA571111 DNA encod	C 380	18	0.9	1378	5	AA573459	AA573459 DNA encod
C 308	18	0.9	1056	8	ACA48714	Aca48714 Prokaryot	C 381	18	0.9	1382	5	AA574298	AA574298 DNA encod
C 309	18	0.9	1060	8	ACA48714	Aca48714 Prokaryot	C 382	18	0.9	1387	5	AA583016	AA583016 DNA encod
C 310	18	0.9	1074	5	AA566375	AA566375 DNA encod	C 383	18	0.9	1395	5	AA577085	AA577085 DNA encod
C 311	18	0.9	1080	5	AA571779	AA571779 DNA encod	C 384	18	0.9	1395	5	AA577941	AA577941 DNA encod
C 312	18	0.9	1095	5	AA578001	AA578001 DNA encod	C 385	18	0.9	1395	5	AA575885	AA575885 DNA encod

C 532	18	0.9	1871	8	ABX98805	Abx98805	Novel hum	C 605	18	0.9	1871	9	ACF24250	ACF24250	Human sec
C 533	18	0.9	1871	8	ACA67316	ACA67316	CDNA enco	C 606	18	0.9	1871	9	ACF63561	ACF63561	Human sec
C 534	18	0.9	1871	8	ACC81282	ACC81282	Human sec	C 607	18	0.9	1871	9	ACF50435	ACF50435	Human sec
C 535	18	0.9	1871	8	ACA95606	ACA95606	Novel hum	C 608	18	0.9	1871	9	ACH07906	ACH07906	Human sec
C 536	18	0.9	1871	8	ACD04524	ACD04524	Novel hum	C 609	18	0.9	1871	9	ACF13712	ACF13712	Human sec
C 537	18	0.9	1871	8	ACC87965	ACC87965	Human sec	C 610	18	0.9	1871	9	ACD41638	ACD41638	Human sec
C 538	18	0.9	1871	8	ACF12627	ACF12627	Human sec	C 611	18	0.9	1871	9	ACF32051	ACF32051	Human sec
C 539	18	0.9	1871	8	ACH66289	ACH66289	Novel hum	C 612	18	0.9	1871	9	ACF32329	ACF32329	Human sec
C 540	18	0.9	1871	8	ACA96342	ACA96342	Novel hum	C 613	18	0.9	1871	9	ACF40019	ACF40019	Human sec
C 541	18	0.9	1871	8	ACA65116	ACA65116	Human PRO	C 614	18	0.9	1871	9	ACD45541	ACD45541	Human sec
C 542	18	0.9	1871	8	ACA73842	ACA73842	Human PRO	C 615	18	0.9	1871	9	ACF53198	ACF53198	Human sec
C 543	18	0.9	1871	8	ACA74254	ACA74254	Novel hum	C 616	18	0.9	1871	9	ACF27378	ACF27378	Human sec
C 544	18	0.9	1871	8	ACA96649	ACA96649	Human PRO	C 617	18	0.9	1871	9	ACF45216	ACF45216	Human sec
C 545	18	0.9	1871	8	ACD10755	ACD10755	CDNA enco	C 618	18	0.9	1871	9	ACF29834	ACF29834	Human sec
C 546	18	0.9	1871	8	ACC91451	ACC91451	Human sec	C 619	18	0.9	1871	9	ACD89910	ACD89910	Human sec
C 547	18	0.9	1871	8	ACD02786	ACD02786	CDNA enco	C 620	18	0.9	1871	9	ACD84691	ACD84691	Human PRO
C 548	18	0.9	1871	8	ACC87351	ACC87351	Human sec	C 621	18	0.9	1871	9	ACD98851	ACD98851	CDNA enco
C 549	18	0.9	1871	8	ACC85935	ACC85935	Human sec	C 622	18	0.9	1871	9	ACF77143	ACF77143	Human sec
C 550	18	0.9	1871	8	ACA65423	ACA65423	Human PRO	C 623	18	0.9	1871	9	ACF76836	ACF76836	Human sec
C 551	18	0.9	1871	8	ACA94240	ACA94240	Human sec	C 624	18	0.9	1871	9	ACF49821	ACF49821	Human sec
C 552	18	0.9	1871	8	ACA97984	ACA97984	Human PRO	C 625	18	0.9	1871	9	ACF50128	ACF50128	Human sec
C 553	18	0.9	1871	8	ACA91486	ACA91486	Novel hum	C 626	18	0.9	1871	9	ACD09527	ACD09527	Human sec
C 554	18	0.9	1871	8	ACA90700	ACA90700	Novel hum	C 627	18	0.9	1871	9	ACD08606	ACD08606	Human sec
C 555	18	0.9	1871	8	ACD16247	ACD16247	Human sec	C 628	18	0.9	1871	9	ACH03621	ACH03621	Human sec
C 556	18	0.9	1871	8	ACD17408	ACD17408	Human sec	C 629	18	0.9	1871	9	ACF12320	ACF12320	Human sec
C 557	18	0.9	1871	8	ACC92065	ACC92065	Human sec	C 630	18	0.9	1871	9	ACC94828	ACC94828	Human sec
C 558	18	0.9	1871	8	ACD02343	ACD02343	Novel hum	C 631	18	0.9	1871	9	ACD22547	ACD22547	Human sec
C 559	18	0.9	1871	8	ACA74922	ACA74922	CDNA enco	C 632	18	0.9	1871	9	ACF15247	ACF15247	Human sec
C 560	18	0.9	1871	8	ACA91793	ACA91793	Human PRO	C 633	18	0.9	1871	9	ACC97342	ACC97342	Human sec
C 561	18	0.9	1871	8	ACA89334	ACA89334	Novel hum	C 634	18	0.9	1871	9	ACC92372	ACC92372	Human sec
C 562	18	0.9	1871	8	ACA71437	ACA71437	Human sec	C 635	18	0.9	1871	9	ACF14019	ACF14019	Human sec
C 563	18	0.9	1871	8	ACC90837	ACC90837	Human sec	C 636	18	0.9	1871	9	ACF14326	ACF14326	Human sec
C 564	18	0.9	1871	8	ACA65847	ACA65847	CDNA enco	C 637	18	0.9	1871	9	ACF09557	ACF09557	Human sec
C 565	18	0.9	1871	8	ACA68971	ACA68971	Novel hum	C 638	18	0.9	1871	9	ACD68394	ACD68394	Novel hum
C 566	18	0.9	1871	8	ACA94992	ACA94992	CDNA enco	C 639	18	0.9	1871	9	ACD45848	ACD45848	Human sec
C 567	18	0.9	1871	8	ACD16554	ACD16554	Human sec	C 640	18	0.9	1871	9	ACD47997	ACD47997	Human sec
C 568	18	0.9	1871	8	ACD15633	ACD15633	Human sec	C 641	18	0.9	1871	9	ACD67728	ACD67728	CDNA enco
C 569	18	0.9	1871	8	ACA98493	ACA98493	Human PRO	C 642	18	0.9	1871	9	ACF25536	ACF25536	Human sec
C 570	18	0.9	1871	8	ABX16736	ABX16736	Human CDN	C 643	18	0.9	1871	9	ACF29230	ACF29230	Human sec
C 571	18	0.9	1871	8	ACA63418	ACA63418	CDNA enco	C 644	18	0.9	1871	9	ACD84998	ACD84998	Human sec
C 572	18	0.9	1871	9	ACA97677	ACA97677	Human PRO	C 645	18	0.9	1871	9	ACD84077	ACD84077	Human PRO
C 573	18	0.9	1871	9	ACA99126	ACA99126	Novel hum	C 646	18	0.9	1871	9	ACD88068	ACD88068	Human sec
C 574	18	0.9	1871	9	ACC91758	ACC91758	Human sec	C 647	18	0.9	1871	9	ACF30755	ACF30755	Human sec
C 575	18	0.9	1871	9	ACD11169	ACD11169	Novel hum	C 648	18	0.9	1871	9	ACF32358	ACF32358	Human sec
C 576	18	0.9	1871	9	ACD15019	ACD15019	Human sec	C 649	18	0.9	1871	9	ACH12018	ACH12018	CDNA enco
C 577	18	0.9	1871	9	ACD11783	ACD11783	Human sec	C 650	18	0.9	1871	9	ACH12325	ACH12325	CDNA enco
C 578	18	0.9	1871	9	ACC95912	ACC95912	Human sec	C 651	18	0.9	1871	9	ADAI1953	ADAI1953	Novel hum
C 579	18	0.9	1871	9	ACF16475	ACF16475	Human sec	C 652	18	0.9	1871	9	ACD40717	ACD40717	Human sec
C 580	18	0.9	1871	9	ACF02593	ACF02593	Human sec	C 653	18	0.9	1871	9	ADBI17336	ADBI17336	Human CDN
C 581	18	0.9	1871	9	ACF02900	ACF02900	Human sec	C 654	18	0.9	1871	9	ACF18189	ACF18189	Human sec
C 582	18	0.9	1871	9	ACF21487	ACF21487	Human sec	C 655	18	0.9	1871	9	ACF08636	ACF08636	Human sec
C 583	18	0.9	1871	9	ACF10171	ACF10171	Human sec	C 656	18	0.9	1871	9	ACF31437	ACF31437	Human sec
C 584	18	0.9	1871	9	ACF78064	ACF78064	Human sec	C 657	18	0.9	1871	9	ACF52277	ACF52277	Human sec
C 585	18	0.9	1871	9	ACD46769	ACD46769	Human sec	C 658	18	0.9	1871	9	ACD50146	ACD50146	Human sec
C 586	18	0.9	1871	9	ACD49532	ACD49532	Human sec	C 659	18	0.9	1871	9	ACF38849	ACF38849	Human sec
C 587	18	0.9	1871	9	ACF28239	ACF28239	Human sec	C 660	18	0.9	1871	9	ACF26764	ACF26764	Human sec
C 588	18	0.9	1871	9	ACD88989	ACD88989	Human sec	C 661	18	0.9	1871	9	ACF24864	ACF24864	Human sec
C 589	18	0.9	1871	9	ACD84384	ACD84384	Human PRO	C 662	18	0.9	1871	9	ACF46444	ACF46444	Human sec
C 590	18	0.9	1871	9	ACD99158	ACD99158	CDNA enco	C 663	18	0.9	1871	9	ACF27992	ACF27992	Human sec
C 591	18	0.9	1871	9	ADA78053	ADA78053	Human sec	C 664	18	0.9	1871	9	ACD89296	ACD89296	Human sec
C 592	18	0.9	1871	9	ACF48900	ACF48900	Human sec	C 665	18	0.9	1871	9	ACF63868	ACF63868	Human sec
C 593	18	0.9	1871	9	ACD09220	ACD09220	Human sec	C 666	18	0.9	1871	9	ACF60508	ACF60508	Human sec
C 594	18	0.9	1871	9	ACF12013	ACF12013	Human sec	C 667	18	0.9	1871	9	ACH12632	ACH12632	CDNA enco
C 595	18	0.9	1871	9	ACF41247	ACF41247	Human sec	C 668	18	0.9	1871	9	ACH10055	ACH10055	Human sec
C 596	18	0.9	1871	9	ACF15861	ACF15861	Human sec	C 669	18	0.9	1871	9	ACD03910	ACD03910	Human sec
C 597	18	0.9	1871	9	ACF16168	ACF16168	Human sec	C 670	18	0.9	1871	9	ACD10448	ACD10448	Human sec
C 598	18	0.9	1871	9	ADBI17148	ADBI17148	Human CDN	C 671	18	0.9	1871	9	ACD12090	ACD12090	Human sec
C 599	18	0.9	1871	9	ACD31995	ACD31995	Human sec	C 672	18	0.9	1871	9	ACF42475	ACF42475	Human sec
C 600	18	0.9	1871	9	ACF18803	ACF18803	Human sec	C 673	18	0.9	1871	9	ACF18496	ACF18496	Human sec
C 601	18	0.9	1871	9	ACF09250	ACF09250	Human sec	C 674	18	0.9	1871	9	ACF02286	ACF02286	Human sec
C 602	18	0.9	1871	9	ACF78371	ACF78371	Human sec	C 675	18	0.9	1871	9	ACF21794	ACF21794	Human sec
C 603	18	0.9	1871	9	ACF51970	ACF51970	Human sec	C 676	18	0.9	1871	9	ACF10478	ACF10478	Human sec
C 604	18	0.9	1871	9	ACF26457	ACF26457	Human sec	C 677	18	0.9	1871	9	ACF33930	ACF33930	Human sec

C 824	18	0.9	1871	9	ACC90421	ACC90421 Human sec	C 897	18	0.9	1871	10	ADCI17226	ADCI17226 cDNA sequ
C 825	18	0.9	1871	9	ACFI10785	ACFI10785 Human sec	C 898	18	0.9	1871	10	ADCI4924	ADCI4924 Novel hum
C 826	18	0.9	1871	9	ACG3600	ACG3600 Human sec	C 899	18	0.9	1871	10	ADCS2419	ADCS2419 Novel hum
C 827	18	0.9	1871	9	ACG96219	ACG96219 Human sec	C 900	18	0.9	1871	10	ADPO5774	ADPO5774 Human sec
C 828	18	0.9	1871	9	ACD24894	ACD24894 Human sec	C 901	18	0.9	1871	10	ADD70732	ADD70732 Human sec
C 829	18	0.9	1871	9	ACF01979	ACF01979 Human sec	C 902	18	0.9	1871	10	ADD39809	ADD39809 Human sec
C 830	18	0.9	1871	9	ACF22101	ACF22101 Human sec	C 903	18	0.9	1871	10	ADD70255	ADD70255 Human sec
C 831	18	0.9	1871	9	ACF22715	ACF22715 Human sec	C 904	18	0.9	1871	10	ADD36095	ADD36095 Novel hum
C 832	18	0.9	1871	9	ACFP08943	ACFP08943 Human sec	C 905	18	0.9	1871	10	ADD38376	ADD38376 Human sec
C 833	18	0.9	1871	9	ACFP3279	ACFP3279 Human sec	C 906	18	0.9	1871	10	ADD39332	ADD39332 Human sec
C 834	18	0.9	1871	9	ACF54733	ACF54733 Human sec	C 907	18	0.9	1871	10	ADD38855	ADD38855 Human sec
C 835	18	0.9	1871	9	ACF48593	ACF48593 Human sec	C 908	18	0.9	1871	10	ADD40286	ADD40286 Human sec
C 836	18	0.9	1871	9	ACD47383	ACD47383 Human sec	C 909	18	0.9	1871	10	ADDS0507	ADDS0507 Human sec
C 837	18	0.9	1871	9	ACD49225	ACD49225 Human sec	C 910	18	0.9	1871	10	ADDS00139	ADDS00139 Human sec
C 838	18	0.9	1871	9	ACF37928	ACF37928 Human sec	C 911	18	0.9	1871	10	ADDS00030	ADDS00030 Human sec
C 839	18	0.9	1871	9	ACF30141	ACF30141 Human sec	C 912	18	0.9	1871	10	ADDS21588	ADDS21588 Human sec
C 840	18	0.9	1871	9	ACD87454	ACD87454 Human sec	C 913	18	0.9	1871	10	ADFS0013	ADFS0013 Human sec
C 841	18	0.9	1871	9	ACF62043	ACF62043 Human sec	C 914	18	0.9	1871	10	ADFS5906	ADFS5906 Human sec
C 842	18	0.9	1871	9	ACH10976	ACH10976 Human sec	C 915	18	0.9	1871	10	ADG01096	ADG01096 Novel hum
C 843	18	0.9	1871	9	ACD10141	ACD10141 Human sec	C 916	18	0.9	1871	10	ADG08649	ADG08649 Novel hum
C 844	18	0.9	1871	9	ACD16866	ACD16866 cDNA enco	C 917	18	0.9	1871	10	ADG02769	ADG02769 Novel hum
C 845	18	0.9	1871	9	ACG99163	ACG99163 Human sec	C 918	18	0.9	1871	10	ADG01476	ADG01476 Novel hum
C 846	18	0.9	1871	9	ACF00557	ACF00557 Human sec	C 919	18	0.9	1871	10	ADP95651	ADP95651 Novel hum
C 847	18	0.9	1871	9	ACD41024	ACD41024 Human sec	C 920	18	0.9	1871	10	ADP95270	ADP95270 Novel hum
C 848	18	0.9	1871	9	ACFI14633	ACFI14633 Human sec	C 921	18	0.9	1871	10	ADG12466	ADG12466 Novel hum
C 849	18	0.9	1871	9	ACF22408	ACF22408 Human sec	C 922	18	0.9	1871	10	ADH24123	ADH24123 Novel hum
C 850	18	0.9	1871	9	ACF78985	ACF78985 Human sec	C 923	18	0.9	1871	10	ADH34149	ADH34149 Novel hum
C 851	18	0.9	1871	9	ACD68040	ACD68040 Novel hum	C 924	18	0.9	1871	10	ADH29982	ADH29982 Novel hum
C 852	18	0.9	1871	9	ACFI1706	ACFI1706 Human sec	C 925	18	0.9	1871	10	ADH23953	ADH23953 Novel hum
C 853	18	0.9	1871	9	ACF51663	ACF51663 Human sec	C 926	18	0.9	1871	10	ADH09126	ADH09126 Novel hum
C 854	18	0.9	1871	9	ACF33586	ACF33586 Human sec	C 927	18	0.9	1871	10	ADG85357	ADG85357 Novel hum
C 855	18	0.9	1871	9	ACD49839	ACD49839 Human sec	C 928	18	0.9	1871	10	ADH24633	ADH24633 Novel hum
C 856	18	0.9	1871	9	ACF37621	ACF37621 Human sec	C 929	18	0.9	1871	10	ADH37489	ADH37489 Novel hum
C 857	18	0.9	1871	9	ACF28606	ACF28606 Human sec	C 930	18	0.9	1871	10	ADH02078	ADH02078 Human sec
C 858	18	0.9	1871	9	ACD88682	ACD88682 Human sec	C 931	18	0.9	1871	10	ADH37659	ADH37659 Novel hum
C 859	18	0.9	1871	9	ACF75301	ACF75301 Human sec	C 932	18	0.9	1871	10	ADG85697	ADG85697 Novel hum
C 860	18	0.9	1871	9	ACF61122	ACF61122 Human sec	C 933	18	0.9	1871	10	ADH24293	ADH24293 Novel hum
C 861	18	0.9	1871	9	ACF44278	ACF44278 Human sec	C 934	18	0.9	1871	10	ADH38587	ADH38587 Novel hum
C 862	18	0.9	1871	9	ACH08520	ACH08520 Human sec	C 935	18	0.9	1871	10	ADG83708	ADG83708 Human sec
C 863	18	0.9	1871	9	ACG39307	ACG39307 Human sec	C 936	18	0.9	1871	10	ADH29516	ADH29516 Novel hum
C 864	18	0.9	1871	9	ACD21012	ACD21012 Human sec	C 937	18	0.9	1871	10	ADH27632	ADH27632 Novel hum
C 865	18	0.9	1871	9	ACF06794	ACF06794 Human sec	C 938	18	0.9	1871	10	ADH37829	ADH37829 Human sec
C 866	18	0.9	1871	9	ACD20705	ACD20705 Human sec	C 939	18	0.9	1871	10	ADH38006	ADH38006 Human sec
C 867	18	0.9	1871	9	ACD22854	ACD22854 Human sec	C 940	18	0.9	1871	10	ADH57426	ADH57426 Novel hum
C 868	18	0.9	1871	9	ACF41554	ACF41554 Human sec	C 941	18	0.9	1871	10	ADH53568	ADH53568 Novel hum
C 869	18	0.9	1871	9	ACF07101	ACF07101 Human sec	C 942	18	0.9	1871	10	ADH53738	ADH53738 Novel hum
C 870	18	0.9	1871	9	ACF77757	ACF77757 Human sec	C 943	18	0.9	1871	10	ADH52074	ADH52074 Novel hum
C 871	18	0.9	1871	9	ACD46155	ACD46155 Human sec	C 944	18	0.9	1871	10	ADH49929	ADH49929 Novel hum
C 872	18	0.9	1871	9	ACF47058	ACF47058 Human sec	C 945	18	0.9	1871	10	ADH25439	ADH25439 Novel hum
C 873	18	0.9	1871	9	ACF54426	ACF54426 Human sec	C 946	18	0.9	1871	10	ADH90232	ADH90232 Novel hum
C 874	18	0.9	1871	9	ACF45830	ACF45830 Human sec	C 947	18	0.9	1871	10	ADH25609	ADH25609 Novel hum
C 875	18	0.9	1871	9	ACF45523	ACF45523 Human sec	C 948	18	0.9	1871	10	ADH97783	ADH97783 Novel hum
C 876	18	0.9	1871	9	ACF38542	ACF38542 Human sec	C 949	18	0.9	1871	10	ADH99410	ADH99410 Human sec
C 877	18	0.9	1871	9	ACD89603	ACD89603 Human sec	C 950	18	0.9	1871	10	ADH93631	ADH93631 Novel hum
C 878	18	0.9	1871	9	ACD85305	ACD85305 Human sec	C 951	18	0.9	1871	10	ADH11988	ADH11988 Human sec
C 879	18	0.9	1871	9	ACD85919	ACD85919 Human sec	C 952	18	0.9	1871	10	ADH90062	ADH90062 Novel hum
C 880	18	0.9	1871	9	ACF75915	ACF75915 Human sec	C 953	18	0.9	1871	10	ADH98463	ADH98463 Novel hum
C 881	18	0.9	1871	9	ACF60815	ACF60815 Human sec	C 954	18	0.9	1871	10	ADH11138	ADH11138 Human sec
C 882	18	0.9	1871	9	ACH05702	ACH05702 cDNA enco	C 955	18	0.9	1871	10	ADH11168	ADH11168 Human sec
C 883	18	0.9	1871	9	ADA82736	ADA82736 Human sec	C 956	18	0.9	1871	10	ADH98293	ADH98293 Novel hum
C 884	18	0.9	1871	9	ADH85664	ADH85664 Novel hum	C 957	18	0.9	1871	10	ADH98633	ADH98633 Novel hum
C 885	18	0.9	1871	9	ACF55961	ACF55961 Human sec	C 958	18	0.9	1871	10	ADH98123	ADH98123 Novel hum
C 886	18	0.9	1871	9	ACF55347	ACF55347 Human sec	C 959	18	0.9	1871	10	ADH78678	ADH78678 Human sec
C 887	18	0.9	1871	10	ADH86044	ADH86044 Human sec	C 960	18	0.9	1871	10	ADH75550	ADH75550 Novel hum
C 888	18	0.9	1871	10	ACF56268	ACF56268 Human sec	C 961	18	0.9	1871	10	ADH71130	ADH71130 Human sec
C 889	18	0.9	1871	10	ACF56575	ACF56575 Human sec	C 962	18	0.9	1871	10	ADH87658	ADH87658 Human sec
C 890	18	0.9	1871	10	ADH68343	ADH68343 Human sec	C 963	18	0.9	1871	10	ADH87044	ADH87044 Human sec
C 891	18	0.9	1871	10	ADH68150	ADH68150 Human sec	C 964	18	0.9	1871	10	ADH04217	ADH04217 Human sec
C 892	18	0.9	1871	10	ACF55654	ACF55654 Human sec	C 965	18	0.9	1871	10	ADH69548	ADH69548 Novel hum
C 893	18	0.9	1871	10	ACF55040	ACF55040 Human sec	C 966	18	0.9	1871	10	ADH90393	ADH90393 Novel hum
C 894	18	0.9	1871	10	ADH90967	ADH90967 Novel hum	C 967	18	0.9	1871	10	ADH89500	ADH89500 Human sec
C 895	18	0.9	1871	10	ADH07047	ADH07047 Human sec	C 968	18	0.9	1871	10	ADH98291	ADH98291 Novel hum
C 896	18	0.9	1871	10	ADH18086	ADH18086 Human sec	C 969	18	0.9	1871	10	ADH93933	ADH93933 Human sec

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FT		/*tag= h
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XX	MO200140271-A2.	
XX		
XX	07-JUN-2001.	
XX		
XX	01-DEC-2000; 2000OWO-US032750.	
XX		
PR	01-DEC-1999; 99US-0168353P.	
PR	26-APR-2000; 2000OUS-00559013.	
XX		
PA	(LUDW-) LUDWIG INST CANCER RES.	
XX		
PI	Ono T, Nakayama E;	
DR	WPI; 2001-397941/42.	
DR	P-FSDB; AAE04382.	
XX		
PT	Isolated polypeptide, useful in treating disorders such as cancer, is	
XX	encoded by a nucleic acid (NA) Group 3 or 4 molecule.	
PS	Claim 56; Fig 2; 127pp; English.	
XX		
CC	The invention relates to cancer associated antigens and their nucleic	
CC	acids which are expressed in methylcholanthrene-induced fibrosarcoma	
CC	cancer cells from mice. Cancer associated antigens and a pharmaceutical	
CC	composition containing nucleic acid molecules encoding cancer associated	
CC	antigens are used to treat a condition e.g. cancer. Cancer associated	
CC	antigens, the nucleotides encoding them. antibodies. Cancer associated	

RESULT 1
AAD08658
ID AAD08658 standard; cDNA; 1895 BP.
XX

[illegible]

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Db      421 CAGCAGTCTCTATTCTCTACCTTACACTCTCAAGAGATGAGAGCTTCAAGTGAAGTC 480
QY      481 TCACCCACCAAGTAGACCTTCCCCATCTCACCCCACTTCAAGTAGACAGACGCCAGACC 540
Db      481 TCACCCACCAAGTAGACCTTCCCCATCTCACCCCACTTCAAGTAGACAGACGCCAGACC 540
QY      541 TTCCAGGCTTGGCTGAGAGGCTTCAAGACACCTGGAAGAGCTCTTCAATCTCTCTTG 600
Db      541 TTCCAGGCTTGGCTGAGAGGCTTCAAGACACCTGGAAGAGCTCTTCAATCTCTCTTG 600
QY      601 TCCCTGGAGAGCCAGAGAGCCAGAGCCAGAGACAGAGAGAGAGAGAGAGAGAGAGAG 660
Db      601 TCCCTGGAGAGCCAGAGAGCCAGAGCCAGAGACAGAGAGAGAGAGAGAGAGAGAGAG 660
QY      661 CAGAGCCGACACAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      661 CAGAGCCGACACAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      721 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db      721 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY      781 GTGCTCAGCTGAGACAGACCTAGAGCCAGAGTTTCACTTGAATCTTCTTCTTAC 840
Db      781 GTGCTCAGCTGAGACAGACCTAGAGCCAGAGTTTCACTTGAATCTTCTTCTTAC 840
QY      841 CCTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
Db      841 CCTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 900
QY      901 ATCCAGAGCTCAATTGATCAGCCAGAGAAATGATGAAATGAAATGATGATGAG 960
Db      901 ATCCAGAGCTCAATTGATCAGCCAGAGAAATGATGAAATGAAATGATGATGAG 960
QY      961 AACTCTTACTGAGAGAAACCAAAACCTCTGAGCTTCTGAGAGCTGCCCCACAGAGGCC 1020
Db      961 AACTCTTACTGAGAGAAACCAAAACCTCTGAGCTTCTGAGAGCTGCCCCACAGAGGCC 1020
QY      1021 TTGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db      1021 TTGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY      1081 GCTGTGAGTATGATGAGAGAGAGAGATCTTGTGAGAGAGTGTGTGTGTGTGTGTGT 1140
Db      1081 GCTGTGAGTATGATGAGAGAGAGAGATCTTGTGAGAGAGTGTGTGTGTGTGTGTGT 1140
QY      1141 GGGCGCGGACATGTTCTACTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
Db      1141 GGGCGCGGACATGTTCTACTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY      1201 TGGCACTCAGAGGCGAGGCTGAGAGGCGACATGAGGCACTTCCCAAGAGCTCCCTTT 1260
Db      1201 TGGCACTCAGAGGCGAGGCTGAGAGGCGACATGAGGCACTTCCCAAGAGCTCCCTTT 1260
QY      1261 GTGAGCCCTTGTGCTTCCAGAGGCTTCCATGCGCAACAGAGTGGGTCCCGAGAA 1320
Db      1261 GTGAGCCCTTGTGCTTCCAGAGGCTTCCATGCGCAACAGAGTGGGTCCCGAGAA 1320
QY      1321 TCAGGCGGCTTTTACGAGGCTGATTTGTGACGTTGGGCTTCCATGCACTTCTGTGTGCC 1380
Db      1321 TCAGGCGGCTTTTACGAGGCTGATTTGTGACGTTGGGCTTCCATGCACTTCTGTGTGCC 1380
QY      1381 CGGCTTGGCCAGAGAGGCTGTGAAGATGTCCAGTCTCTGGGTGGCTCCAGAGCTGAGTTTC 1440
Db      1381 CGGCTTGGCCAGAGAGGCTGTGAAGATGTCCAGTCTCTGGGTGGCTCCAGAGCTGAGTTTC 1440
QY      1441 CTTAGCTTCCAGAGTGGGATTTTCCCTTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
Db      1441 CTTAGCTTCCAGAGTGGGATTTTCCCTTACCAAGATTTGTGACACAGACTATATCCAGTAC 1500
QY      1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGGTG 1560
Db      1501 CCAAACTACTGTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGCAATCGGAAGGTG 1560

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QY      1561 TCCCGATGAGATGTCTGACGAATGAGACTTACAGTGCCTGAGCCCTTGCAAAAGTAG 1620
Db      1561 TCCCGATGAGATGTCTGACGAATGAGACTTACAGTGCCTGAGCCCTTGCAAAAGTAG 1620
QY      1621 GAGGTGTGCTTGTGATGAGAGCCAGAGATTGAGACCTTGAATCTGAGGCCAGTTGGATGA 1680
Db      1621 GAGGTGTGCTTGTGATGAGAGCCAGAGATTGAGACCTTGAATCTGAGGCCAGTTGGATGA 1680
QY      1681 GCTGAGCTTATTTCTGCGCACACCCAGCCCACTGCCCCAGCTTCTTATTTGTTTGTAG 1740
Db      1681 GCTGAGCTTATTTCTGCGCACACCCAGCCCACTGCCCCAGCTTCTTATTTGTTTGTAG 1740
QY      1741 ACCCCATTTCTTCAAGGCTGCCCCCTTGTGAGTCTGTTACTGAGCCCTTACTCAATTTCC 1800
Db      1741 ACCCCATTTCTTCAAGGCTGCCCCCTTGTGAGTCTGTTACTGAGCCCTTACTCAATTTCC 1800
QY      1801 TTGGGTGAGCAACAGTCCCAAGAGAGGCCAGCGTGGAGGCTGCGCTCTTAAAGA 1860
Db      1801 TTGGGTGAGCAACAGTCCCAAGAGAGGCCAGCGTGGAGGCTGCGCTCTTAAAGA 1860
QY      1861 TGACTTTACATTAATCTTGAATCTTCAAAAAA 1895
Db      1861 TGACTTTACATTAATCTTGAATCTTCAAAAAA 1895

RESULT 2
ABT14679
ID ABT14679 standard; DNA; 1886 BP.
XX
AC ABT14679;
XX
DT 27-FEB-2003 (first entry)
XX
DE Human cancer-testis antigen coding sequence #6.
XX
KM Human; gene; de; gene therapy; vaccine; cancer-testis antigen;
XX CT antigen; breast cancer; colon cancer; cervical cancer; gastric cancer.
XX
OS Homo sapiens.
XX
PN W0200286071-A2.
XX
PD 31-OCT-2002.
XX
PF 19-APR-2002; 2002MO-US012497.
XX
PR 20-APR-2001; 2001US-0285343P.
PR 14-FEB-2002; 2002US-0356937P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Nakayama E, Ono T, Old LJ;
XX
DR WPI; 2003-075624/07.
XX
DR P-PADB; AAO16118.
XX
PT New cancer-testis (CT) antigens, nucleic acids and encoded polypeptides,
PT useful for diagnosing, monitoring or treating disorder or condition
PT associated with the expression of human CT antigens, e.g. breast cancer
PT or cervical cancer.
XX
PS Example 2; Page 151-154; 165pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC cancer-testis (CT) antigens that bind an HLA molecule. The CT antigens of
CC the invention are useful for diagnosing, monitoring or treating cancer
CC (e.g. breast cancer, colon cancer, cervical cancer or gastric cancer).
CC The present DNA sequence encodes a human cancer-testis (CT) antigen
XX
SQ Sequence 1886 BP; 440 A; 565 C; 481 G; 400 T; 0 U; 0 Other;
Query Match 99.5%; Score 1886; DB 8; Length 1886;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTAGAGGCGGCTTGTGTCACGGGACGGGCGGATCTTCTCGGCAATGAGAAAGCA 60
Db 1 GTTAGAGGCGGCTTGTGTCACGGGACGGGCGGATCTTCTCGGCAATGAGAAAGCA 60
QY 61 GCGCGTGGCTTCTTCCCTCACTCTGAAAGTGCTGCTGCTTGGCACTTGGCCCA 60
Db 61 GCGCGTGGCTTCTTCCCTCACTCTGAAAGTGCTGCTGCTTGGCACTTGGCCCA 60
QY 121 GCCCAGATTCGACTCAGGCGCCCACTCCAGGAGGCTCTCTCTCAACGAAATGAGAA 180
Db 121 GCCCAGATTCGACTCAGGCGCCCACTCCAGGAGGCTCTCTCTCAACGAAATGAGAA 180
QY 181 GCGTTCTTGGCACTGCTGACTCCAACTGGAAGGAGGAGCACTACCTGCTCTCGTGA 240
Db 181 GCGTTCTTGGCACTGCTGACTCCAACTGGAAGGAGGAGCACTACCTGCTCTCGTGA 240
QY 241 ACCCAGGCTGCGGGAATCCCACTCTGCTGCACTGGAACAAATGAAAAACAAGGCTTA 300
Db 241 ACCCAGGCTGCGGGAATCCCACTCTGCTGCACTGGAACAAATGAAAAACAAGGCTTA 300
QY 301 GTGCGGATGATGCTGTCTGCTCCAACTCTCTTATGCTCTGCTTGAATCTTCTGTC 360
Db 301 GTGCGGATGATGCTGTCTGCTCCAACTCTCTTATGCTCTGCTTGAATCTTCTGTC 360
QY 361 CAGTTCACTGACTACCGTTGCTCCAACTGCTACTATGCTCAAGAGAGTCTGTTGCC 420
Db 361 CAGTTCACTGACTACCGTTGCTCCAACTGCTACTATGCTCAAGAGAGTCTGTTGCC 420
QY 421 CAGCAGTCTCTATTTCTCTCACTTCACTCTCAAGAGATGAAAGCTTCACTGAAATC 480
Db 421 CAGCAGTCTCTATTTCTCTCACTTCACTCTCAAGAGATGAAAGCTTCACTGAAATC 480
QY 481 TCACCCACACAGATGACTTCCCATCTCACTCAAGAGATGAAAGCTTCACTGAAATC 480
Db 481 TCACCCACACAGATGACTTCCCATCTCACTCAAGAGATGAAAGCTTCACTGAAATC 480
QY 541 TTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 TCCCTGGAGGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 TCCCTGGAGGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CAGGAGCGGACACAAAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 661 CAGGAGCGGACACAAAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GAACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 GAACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 GTGTCTCAGCTGACAGACAGACTCAGAGCCCAAGTTCACTCTGAATCTCTATCTTAC 840
Db 781 GTGTCTCAGCTGACAGACAGACTCAGAGCCCAAGTTCACTCTGAATCTCTATCTTAC 840
QY 841 CTTTCTCTTTTGTCTCCCGGGTAAGAGAGATGAGTCTTCTCTCTCTCTCTCTCTCT 900
Db 841 CTTTCTCTTTTGTCTCCCGGGTAAGAGAGATGAGTCTTCTCTCTCTCTCTCTCTCT 900
QY 901 ATCCAGAGGCTATTTGATCAGCCAGGAAATGATGAAATGAAATGAAATGAAATGAG 960
Db 901 ATCCAGAGGCTATTTGATCAGCCAGGAAATGATGAAATGAAATGAAATGAAATGAG 960
QY 961 AACTCTTACTGAGAAACCAAACTCTGAGCTTCTGAGCTGCCCCACAGAGGCT 1020
Db 961 AACTCTTACTGAGAAACCAAACTCTGAGCTTCTGAGCTGCCCCACAGAGGCT 1020
QY 1021 TTGCTGTCTCTGCTATTTGATGATGAGAAATACCTGATCTAATACCCCAAGCCAG 1080
Db 1021 TTGCTGTCTCTGCTATTTGATGATGAGAAATACCTGATCTAATACCCCAAGCCAG 1080

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Db 1021 TTGCTGTCTCTGCTATTTGATGATGAGAAATACCTGATCTAATACCCCAAGCCAG 1080
QY 1081 GCTTGAAAGTACATGAGAGAGAGATCTTGTGTTTGGGAAAGTGGTCTGTGACAGCTT 1140
Db 1081 GCTTGAAAGTACATGAGAGAGAGATCTTGTGTTTGGGAAAGTGGTCTGTGACAGCTT 1140
QY 1141 GGGCGGCGACACATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1141 GGGCGGCGACACATGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1201 TGCACTCAGAGGCGACGCTGCAAGCGGCAACATGAGACACCTCCCAAGACTCTCTT 1260
Db 1201 TGCACTCAGAGGCGACGCTGCAAGCGGCAACATGAGACACCTCCCAAGACTCTCTT 1260
QY 1261 GTCAGCCCTTGTCTTCTCTCCAGAGCCTGTCATTCGCAACAGATAGGCTCCAGAA 1320
Db 1261 GTCAGCCCTTGTCTTCTCTCCAGAGCCTGTCATTCGCAACAGATAGGCTCCAGAA 1320
QY 1321 TCAGGCGGCTTTTAAAGGCTGAGATTTGATACGATGAGCTCCCAATGAGCTTCTG 1380
Db 1321 TCAGGCGGCTTTTAAAGGCTGAGATTTGATACGATGAGCTCCCAATGAGCTTCTG 1380
QY 1381 CGGCTTGCCACGAAAGGCTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 CGGCTTGCCACGAAAGGCTGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 CTTAGCTTCCAGAGAGGAGATTTCTCTCAAGATTTGAGACAGAGACTATATCCAGTAC 1500
Db 1441 CTTAGCTTCCAGAGAGGAGATTTCTCTCAAGATTTGAGACAGAGACTATATCCAGTAC 1500
QY 1501 CCAAACTATGCTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGAATGGAAGGTG 1560
Db 1501 CCAAACTATGCTTCTTCAAAAGCCAGAGTGTCTGATGAGAAACCGAATGGAAGGTG 1560
QY 1561 TCCCGATGAGATGCTGCAAGATGAGATTAAGTGTGCTGAGAGCCCTGCAAAAGTGA 1620
Db 1561 TCCCGATGAGATGCTGCAAGATGAGATTAAGTGTGCTGAGAGCCCTGCAAAAGTGA 1620
QY 1621 GAGGTTGTCTGATGAGAGCCAGAGATTCAGACCTTGAACCTGAGCCCTGCAAAAGTGA 1680
Db 1621 GAGGTTGTCTGATGAGAGCCAGAGATTCAGACCTTGAACCTGAGCCCTGCAAAAGTGA 1680
QY 1681 GCTGGGCTTATTTGAGGCGACACCCAGCCCACTGCGCCCTCTATGTTTGAAG 1740
Db 1681 GCTGGGCTTATTTGAGGCGACACCCAGCCCACTGCGCCCTCTATGTTTGAAG 1740
QY 1741 ACCCATGCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 ACCCATGCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
QY 1801 TTGGGTTGAGCAACATCTCCAGAGAGGCGACGAGGAGGCTGCGCCCTCTTAAAGA 1860
Db 1801 TTGGGTTGAGCAACATCTCCAGAGAGGCGACGAGGAGGCTGCGCCCTCTTAAAGA 1860
QY 1861 TGACTTTACATTAATGTTGATCTTC 1886
Db 1861 TGACTTTACATTAATGTTGATCTTC 1886

```

RESULT 2

AA250927 standard; cDNA; 1912 BP.

AA250927;

05-JUN-2000 (first entry)

Human Protease and associated protein-10 (PRG-10) encoding cDNA.

Protease and associated protein-10; PRG-10; anti-PRG antibody;
arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
AIDS; Addison's disease; adult respiratory distress syndrome; allergy;

KW ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
KM hepatocellular; antinflammatory; virucide; antiparasitic; anti-HIV;
KM allergic; immunosuppressive; antidiabetic; antianemic;
KM neuroprotective; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1696
FT /tag= a
FT /product= "Human PPRG-10"
FT sig_peptide 65..139
FT /tag= b
FT mat_peptide 140..1693
FT /tag= c
FT /product= "Mature PPRG-10"
FT misc_binding 1190..1234
FT /tag= d
FT /bound_moiety= "Probe or Primer"
FT
PN MO200009709-A2.
XX 24-FEB-2000.
XX 06-AUG-1999; 99MO-US017818.
XX
PR 10-AUG-1998; 98US-0096114P.
PR 11-FEB-1999; 99US-0119768P.
XX
PA (INCY-) INCYTE PHARM INC.
XX Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;
PI Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;
PI Shih LL, Lu DM;
XX WPI; 2000-224346/19.
DR P-PSDB; AAY70016.
XX
PT New human proteases, useful for diagnosis, treatment and prevention of
PT cell proliferative disorders such as atherosclerosis.
XX
PS Claim 9; Page 106; 114pp; English.
XX
CC The present sequence is a cDNA identified in Incyte clone 1393101 derived
CC from THRN0703 cDNA library. It encodes human protease and associated
CC protein-10 (PPRG-10), which is expressed in reproductive, endocrine,
CC haematopoietic and immune tissues. Anti-PPRG antibodies can be used as
CC therapeutic antagonists, reagents for diagnosis and monitoring diseases
CC and for isolating PPRG. PPRG nucleotide sequence can be used as probe or
CC primer for diagnosis and monitoring of PPRG-related diseases and gene
CC mapping. PPRG can be used in the treatment of cell proliferative
CC disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,
CC cirrhosis and hepatitis, and immune disorders like AIDS, Addison's
CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis and amyloidosis
CC
XX
SQ Sequence 1912 BP; 455 A; 567 C; 487 G; 403 T; 0 U; 0 Other;
Query Match 91.9%; Score 1742; DB 3; Length 1912;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1892; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTTAGAGGGGGCTTGTGTCACGCGGAGCGGGGCGATCTTCGCGCATGAGGAAGCA 60
Db GTTAGAGGGGGCTTGTGTCACGCGGAGCGGGGCGATCTTCGCGCATGAGGAAGCA 76
QY 61 GCGGTGGCTTCTCTCCCTCACTCTGAGAGTGTCTCTGCTTGACACTGCGGCA 120
Db GCGGTGGCTTCTCTCCCTCACTCTGAGAGTGTCTCTGCTTGACACTGCGGCA 136
QY 121 GCCCAGATTGACTCAGGCGCCCACTCCAGGAGCGCTCTCTCTTACCGAATAGAA 180
Db GCCCAGATTGACTCAGGCGCTCCACTCCAGGAGCGCTCTCTCTTACCGAATAGAA 196

QY 181 CGCTTCTTCCGACTGCTGACTCCAACTGGAAGGCAAGACTACCTGCGCTCCGTCGA 240
Db CGCTTCTTCCGACTGCTGACTCCAACTGGAAGGCAAGACTACCTGCGCTCCGTCGA 256
QY 241 ACCCAGGCTGCGGGAATCCCACTGTCGAGCTGAGCAATATGAAAAACAGGCTTA 300
Db ACCCAGGCTGCGGGAATCCCACTGTCGAGCTGAGCAATATGAAAAACAGGCTTA 316
QY 301 GTGCCGATGATGTGTCTGTCTGCTCAACCTCCCTTAATGCTTGTGATCTTCTGC 360
Db GTGCCGATGATGTGTCTGTCTGCTCAACCTCCCTTAATGCTTGTGATCTTCTGC 376
QY 361 CAGTTCACTCACTACCTGTCTCAACCAAGTCTACTATGCAAGAGTCTGTGTTC 420
Db CAGTTCACTCACTACCTGTCTCAACCAAGTCTACTATGCAAGAGTCTGTGTTC 436
QY 421 CAGCGATCTCTATTCTCTCACTCACTCTCAAGAGATAGAGCTTCAAGTGAATGC 480
Db CAGCGATCTCTATTCTCTCACTCACTCTCAAGAGATAGAGCTTCAAGTGAATGC 496
QY 481 TCACCCACAGATGACCTCCCATCTCAACCCCACTTCAAGTGAAGAGAGGCAAGC 540
Db TCACCCACAGATGACCTCCCATCTCAACCCCACTTCAAGTGAAGAGAGGCAAGC 556
QY 541 TTCAGGCTTGGCTGAGAGGCTCAGCAACAGTGAAGAGCTCTACATCTCTCTTG 600
Db TTCAGGCTTGGCTGAGAGGCTCAGCAACAGTGAAGAGCTCTACATCTCTCTTG 616
QY 557 TTCCAGGCTTGGCTGAGAGGCTCAGCAACAGTGAAGAGCTCTACATCTCTCTTG 616
QY 601 TCCCTGGAGGCAAGAGCAAGGCGCAGACAGCAAGAGAGAGAGTGAAGCAGAG 660
Db TCCCTGGAGGCAAGAGCAAGGCGCAGACAGCAAGAGAGAGAGTGAAGCAGAG 676
QY 617 TCCTGGAGGCAAGAGCAAGGCGCAGACAGCAAGAGAGAGAGTGAAGCAGAG 676
QY 661 CAGAGCGGCAACAAGAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db CAGAGCGGCAACAAGAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 736
QY 721 GAAAG 780
Db GAAAG 796
QY 781 GTGCTCAGCTGAGACAGACTGAGAGCCCAAGTTTCACTTGAATCTTATCTTAC 840
Db GTGCTCAGCTGAGACAGACTGAGAGCCCAAGTTTCACTTGAATCTTATCTTAC 856
QY 841 CTTTCTCTTTTGTCTCCCGGATACAGAGATGATCTCTCTATGATATGAGAAC 900
Db CTTTCTCTTTTGTCTCCCGGATACAGAGATGATCTCTCTATGATATGAGAAC 916
QY 901 ATCCAGAGGCTCATTCGATCAGCCAGAGAAATGATGAATGATATGATGAG 960
Db ATCCAGAGGCTCATTCGATCAGCCAGAGAAATGATGAATGATATGATGAG 976
QY 917 ATCCAGAGGCTCATTCGATCAGCCAGAGAAATGATGAATGATATGATGAG 976
QY 961 AACTCTACTGAGAAACCAAAACCTTGAGCTTCTGAGCTGCCCAACAGAGGCC 1020
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QY 977 AACTCTACTGAGAAACCAAAACCTTGAGCTTCTGAGCTGCCCAACAGAGGCC 1036
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QY 1037 TTGCTGTGTGTGTCTATTGATGATGATGATGATGATGATGATGATGATGATG 1096
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QY 1097 GCTTGAAGTACATGAGAGAGAGATCTTGTGTTGGAGAGTCCGCTGACAGCTT 1156
QY 1141 GGGGCGGACACATGCTTACCTGTGCTTGTGATCTTGTCTTGAAGCTGAGCAG 1200
Db GGGGCGGACACATGCTTACCTGTGCTTGTGATCTTGTCTTGAAGCTGAGCAG 1216
QY 1157 GGGGCGGACACATGCTTACCTGTGCTTGTGATCTTGTCTTGAAGCTGAGCAG 1216
QY 1201 TGCACATCAAGAGCGCGCTGAGCGGCAACATGAGCAACCTCCCAAGAGCTCCCTT 1260
Db TGCACATCAAGAGCGCGCTGAGCGGCAACATGAGCAACCTCCCAAGAGCTCCCTT 1276

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QY 1261 GTGAGCCCTTCTGCTCCAGAGCCGTCATCCGAGCAAGGTTAGGCTCCCGAGAA 1320
DB 1277 GTGAGCCCTTCTGCTCCAGAGCCGTCATCCGAGCAAGGTTAGGCTCCCGAGAA 1336
QY 1321 TCAGGCGGCTTTTACGGCTGGATTGTGACGGTGGGCTCCAGATGACTTCTGGTGGCC 1380
DB 1337 TCAGGCGGCTTTTACGGCTGGATTGTGACGGTGGGCTCCAGATGACTTCTGGTGGCC 1396
QY 1381 CGGCTTGCACGAAAGGCTGTGAAGATGTCGCAATCTCTGGTGGCTCCAGACTGATTC 1440
DB 1397 CGGCTTGCACGAAAGGCTGTGAAGATGTCGCAATCTCTGGTGGCTCCAGACTGATTC 1456
QY 1441 CTTGCTTCCAGATGGGAGATTCTCCAGAGATTGTGACACAGACTATATCCAGTAC 1500
DB 1457 CTTGCTTCCAGATGGGAGATTCTCCAGAGATTGTGACACAGACTATATCCAGTAC 1516
QY 1501 CCAAACTACTGTTCTCTCAAAAGCCAGACTGTCTGATGAAACCGCAATCGAAGGTG 1560
DB 1517 CCAAACTACTGTTCTCTCAAAAGCCAGACTGTCTGATGAAACCGCAATCGAAGGTG 1576
QY 1561 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTCCGCTGAGCCCTGGCAAAAGTAC 1620
DB 1577 TCCCGCATGAGATGTCTGCAAGATGAGACTTACAGTCCGCTGAGCCCTGGCAAAAGTAC 1636
QY 1621 GAGCTTGTGCTGATGAGAGCCAGAGTTCAGACCTTGACTTGAAGCCAGTTGGATGA 1680
DB 1637 GAGCTTGTGCTGATGAGAGCCAGAGTTCAGACCTTGACTTGAAGCCAGTTGGATGA 1696
QY 1681 GCTGGGCTTATTTCTGCCACACCCAGAGCCCAACTGCTCCGATTTGTTTGGAG 1740
DB 1697 GCTGGGCTTATTTCTGCCACACCCAGAGCCCAACTGCTCCGATTTGTTTGGAG 1756
QY 1741 ACCCATGCTTTCAGAGCTGCCCTTCTGGGCTGTCTTACTGGGCCCTTACATTCATTC 1800
DB 1757 ACCCATGCTTTCAGAGCTGCCCTTCTGGGCTGTCTTACTGGGCCCTTACATTCATTC 1816
QY 1801 TTGGGTTGAGCAACAGTCCAGAGAGGCGCACGTTGGAGACTGGCCCTTAAAGAA 1860
DB 1817 TTGGGTTGAGCAACAGTCCAGAGAGGCGCACGTTGGAGACTGGCCCTTAAAGAA 1876
QY 1861 TGACTTTACATTAATGTTGATCTTCAAAAAA 1895
DB 1877 TGACTTTACATTAATGTTGATCTTCAAAAAA 1911

RESULT 4
AAK06785
ID AAK06785 standard; cDNA, 1899 BP.
AC AAK06785;
XX
DT 26-APR-1999 (first entry)
XX
DE Human adult testis secreted protein ga63_6 cDNA.
XX
KW Secreted protein; human; testis; ga63_6; ds.
XX
OS Homo sapiens.
XX
FH Key Location/qualifiers
FT CDS 43..1674
FT FT /tag= a
FT FT /note= "this region (minus the stop codon at 1672..1674)
FT FT is specifically claimed in Claim 24(b)"
FT FT sig_peptide /tag= b
FT FT /product= "putative leader/signal sequence, or
FT FT transmembrane region"
FT FT mat_peptide /tag= c
FT FT /note= "this region is specifically claimed in Claim
FT FT 24(c)"
FT misc_feature 224..679

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FT FT /*tag= d
FT FT /note= "this region is specifically claimed in Claim
FT FT 24(d)"
PN W09857976-A1.
PD 23-DEC-1998.
XX
XX 18-JUN-1998; 98WO-US012516.
PF 19-JUN-1997; 97US-00878715.
PR 17-JUN-1998; 98US-00098588.
XX
XX (GENY) GENETICS INST INC.
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Treacy M, Spaulding V;
PI Agostino MJ, Howes SH, Fichtel K,
XX WPI; 1999-095321/08.
XX P-PSDB; AAM88403.
XX
XX New polynucleotides encoding secreted human proteins - are derived from
XX human foetal brain, adult testes, adult uterus, adult trachea or adult
XX neural tissue cDNA libraries, used as, e.g. vaccines.
PS Claim 24(a); Page 84-85; 122pp; English.
XX
XX This cDNA clone, termed ga63_6, codes for a novel human secreted protein
XX (see AAM88403). The full-length clone was isolated from a human adult
XX testis cDNA library using methods which are selective for cDNAs encoding
XX secreted proteins, or was identified as encoding a secreted or
XX transmembrane protein on the basis of computer analysis of the amino acid
XX sequence of the encoded protein. Its sequence shows at least some
XX similarity to some known database sequences. The invention provides cDNA
XX clones (see AAK06780-89) from human adult testis, foetal brain, adult
XX uterus, adult trachea and adult neural tissue that encode novel secreted
XX proteins (see AAM89398-407). The clones are deposited as ATCC 98468, from
XX which each can be isolated using specified probes (see AAK06790-99). The
XX polynucleotides and proteins are predicted to have biological activities
XX which would make them suitable for treating, preventing or ameliorating
XX medical conditions in humans and animals, although no supporting data is
XX given. Suggested activities include nutritional, cytokine, cell
XX proliferation/differentiation, immune stimulating (e.g. as vaccines) or
XX suppressing, haematopoiesis regulation, tissue growth, activin or
XX inhibin, chemotactic or chemokinetic, haemostatic, thrombolytic activity,
XX receptor/ligand, antiinflammatory, cadherin/tumour invasion suppressor,
XX CC and tumour inhibition activities. The polynucleotides are also stated to
XX be useful for gene therapy, and for recombinant production of the claimed
XX proteins
XX
XX Sequence 1899 BP; 457 A; 560 C; 477 G; 401 T; 0 U; 4 Other;
SQ
Query Match 78.8%; Score 1494; DB 2; Length 1899;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCTTGTGTCACGAGACGCGGCGGATCTTCTCGGCCATGAGAAAGCAGCCGTGGCT 70
DB 5 GCTTGTGTCACGAGACGCGGCGGATCTTCTCGGCCATGAGAAAGCAGCCGTGGCT 64
QY 71 TCCCTCCCTCACCTCCGAAAGGCTGCTCTGCTCTGCTGCGACCTGCGCAGCCAGATT 130
DB 65 TCCCTCCCTCACCTCCGAAAGGCTGCTCTGCTCTGCTGCGACCTGCGCAGCCAGATT 124
QY 131 CGACTGAGGCCCCCAGCTCCAGGAGCCCTCTCTCCCTACCGAATAGAACGCTTCTTG 190
DB 125 CGACTGAGGCCCCCAGCTCCAGGAGCCCTCTCTCTCCCTACCGAATAGAACGCTTCTTG 184
QY 191 CACTGCTACTCCCACTCTGAAAGGAGAGACTTACCTGCTCTCTGCAACCAAGGCT 250
DB 185 CACTGCTACTCCCACTCTGAAAGGAGAGACTTACCTGCTCTCTGCAACCAAGGCT 244
QY 251 GCCGGAATCCCACTGCTCAGCTGAGCAATATGAAAACAGAGGCTTAGTGGCCGATG 310

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Db      245 GCGGATATCCACAACCTGCTCAGCTGAGCAAAATGAAAACAAGGCTTATGTCCTCATG
Qy      311 GTGCTGTCTGCTCAACCTCCTTATGCTCTGTGTTGAGCTTTTGTGCAAGTTCACTC
Db      305 GTGCTGTCTGCTCAACCTCCTTATGCTCTGTGTTGAGCTTTTGTGCAAGTTCACTC
Qy      371 ACTACGGTGTCTCAACCTGCTTACTATGCAAGAGAGTCTGTGTTTCCCAAGCACTC
Db      365 ACTACGGTGTCTCAACCTGCTTACTATGCAAGAGAGTCTGTGTTTCCCAAGCACTC
Qy      431 CATTTCTTCACTTAACCTTCAAGAGATAGAGAGTTGAGTGTGAGTCTCAACCA
Db      425 CATTTCTTCACTTAACCTTCAAGAGATAGAGAGTTGAGTGTGAGTCTCAACCA
Qy      491 CGATGACCTCCCATCTCAACCTTCAAGTACAGAGCAAGAGCAAGTCTTCAAGCTT
Db      485 CGATGACCTCCCATCTCAACCTTCAAGTACAGAGCAAGAGCAAGTCTTCAAGCTT
Qy      551 GGCCTGAGAGGCTCAGCAACAGTGAAGAGCTCTCAATCCTCTTGTCCCTGGAG
Db      545 GGCCTGAGAGGCTCAGCAACAGTGAAGAGCTCTCAATCCTCTTGTCCCTGGAG
Qy      611 GCCAGAGAGCAAGGCGCAGAGCAACAGAGAGAGTGTGAGCAGAGCAAGAGCGA
Db      605 GCCAGAGAGCAAGGCGCAGAGCAACAGAGAGAGTGTGAGCAGAGCAAGAGCGA
Qy      671 CACAAGAACACAAGCAGAGAGAGGAGCAAGAGAGCAAGAGAGCAAGAGAG
Db      665 CACAAGAACACAAGCAGAGAGAGGAGCAAGAGAGCAAGAGAGCAAGAGAG
Qy      731 AGAGAGGAAAGCAGAGAGAGAGCAAGAGAGAGGAGGAGGCTGTGTCTCAGC
Db      725 AGAGAGGAAAGCAGAGAGAGAGCAAGAGAGAGGAGGAGGCTGTGTCTCAGC
Qy      791 TGCAGACAACACTCAGAGGCCCAAGTTCTCACTGAAATCTTATCTTCAACCTTCTT
Db      785 TGCAGACAACACTCAGAGGCCCAAGTTCTCACTGAAATCTTATCTTCAACCTTCTT
Qy      851 TTGCTCCCCGGGATCAGAGAGTGAAGTCTTCTTATGAATATGAGAAATCAGAGAGC
Db      845 TTGCTCCCCGGGATCAGAGAGTGAAGTCTTCTTATGAATATGAGAAATCAGAGAGC
Qy      911 TCATTGATCAGCCAGAAATAGATGAATGAATGAATATATATGATGAATCTCTACT
Db      905 TCATTGATCAGCCAGAAATAGATGAATGAATGAATGAATATATGATGAATCTCTACT
Qy      971 GGAAGAAACCAAAACCTTGGCAGCTTCTGCAAGTGTCCCAACAGAGAGCTTGTGTC
Db      965 GGAAGAAACCAAAACCTTGGCAGCTTCTGCAAGTGTCCCAACAGAGAGCTTGTGTC
Qy      1031 TGTGCAATTCGATTCGAGAGAAATCCTGATCATTAACCCCAAGCCAGCTTGAAGT
Db      1025 TGTGCAATTCGATTCGAGAGAAATCCTGATCATTAACCCCAAGCCAGCTTGAAGT
Qy      1091 ACATGAGAGAGAGATCTTGTGTTGCGGAGAGTGGTCTGTGACAGCTTGGCGGAGC
Db      1085 ACATGAGAGAGAGATCTTGTGTTGCGGAGAGTGGTCTGTGACAGCTTGGCGGAGC
Qy      1151 ACATGCTTACCTGTGCTCTGTGACTTGTGCTCTTGAAGCTGAGCAAGTGCACCTCAG
Db      1145 ACATGCTTACCTGTGCTCTGTGACTTGTGCTCTTGAAGCTGAGCAAGTGCACCTCAG
Qy      1211 AGGCGAGCTGAGAGGCGGCAACATGAGACACTTCCCAAGAGTCCCTTGTGACGCCCT
Db      1205 AGGCGAGCTGAGAGGCGGCAACATGAGACACTTCCCAAGAGTCCCTTGTGACGCCCT
Qy      1271 TGCCTGCTTCCAGAGAGCTGTCCATCGGCAACAGGTAAGGCTCCCAAGATCAGGCGCT
Db      1265 TGCCTGCTTCCAGAGAGCTGTCCATCGGCAACAGGTAAGGCTCCCAAGATCAGGCGCT
Qy      1331 TTTTACGGGCTGATTTTGTACGTTGGGCTTCAATGACCTTGTGTTGCGGCTTGCCA

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Db      1325 TTTACGGGCTGATTTTGTACGTTGGGCTCCACATGACCTTGTGTTGCCGCTTCCCA
Qy      1391 CGAAGGCTGTGAAGATGTCGAGTCTGTGGTGGCTCCAGACTGATGTTCTTAGCTTCC
Db      1385 CGAAGGCTGTGAAGATGTCGAGTCTGTGGTGGCTCCAGACTGATGTTCTTAGCTTCC
Qy      1451 AGGATGGGATTTTCCCTTCAACAGATTTTGTGACACAGCTATATTCAGTACCCAACTACT
Db      1445 AGGATGGGATTTTCCCTTCAACAGATTTTGTGACACAGCTATATTCAGTACCCAACTACT
Qy      1511 GTTCTTCAAAACCCAGAGAGTGTCTGATGAGAAACCGCAATCCGGAAGTGTCCGCAATGA
Db      1505 GTTCTTCAAAACCCAGAGAGTGTCTGATGAGAAACCGCAATCCGGAAGTGTCCGCAATGA
Qy      1571 GATGCTGCAGATGAGACTTACAGTGCCTGAGCC 1606
Db      1565 GATGCTGCAGATGAGACTTACAGTGCCTGAGCC 1600

RESULT 5
AAZ24890
ID  AAZ24890 standard; DNA; 1892 BP.
XX
AC  AAZ24890;
XX
DT  02-DEC-1999 (first entry)
XX
DE  Human secreted protein gene 80 clone HUMA54.
XX
KW  Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW  diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW  developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW  immune system; aschima; lymphocytic disease; brain; hepatic; lymphoma;
KW  inflammation; ischaemic shock; Alzheimer's disease; resection; AIDS;
KW  cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW  osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW  endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS  Homo sapiens.
XX
PN  WO947540-A1.
XX
PD  23-SEP-1999.
XX
PF  18-MAR-1999; 99MO-US005804.
XX
PR  19-MAR-1998; 98US-0078563P.
PR  19-MAR-1998; 98US-0078566P.
PR  19-MAR-1998; 98US-0078573P.
PR  19-MAR-1998; 98US-0078574P.
PR  19-MAR-1998; 98US-0078576P.
PR  19-MAR-1998; 98US-0078577P.
PR  19-MAR-1998; 98US-0078578P.
PR  19-MAR-1998; 98US-0078579P.
PR  19-MAR-1998; 98US-0078581P.
PR  01-APR-1998; 98US-0080312P.
PR  01-APR-1998; 98US-0080313P.
PR  01-APR-1998; 98US-0080314P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR;
PI  Wei Y, Endress GA, Duan RD, Kyaw H, Bener R, Lafleur DW, Olsen HS;
PI  Shi Y, Moore PA;
XX
DR  MPI; 1999-562050/47.
XX
P  P-PSDB; AAY41387.
XX
PT  New isolated human genes, useful for diagnosis and treatment of e.g.
PT  cancers, neurological disorders, immune diseases, inflammation or blood
PT  disorders.
XX
PS  Claim 1; Page 346; 484pp; English.

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XX AC ADA39940;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human secreted protein encoding cDNA.
 XX KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytostatic; immunosuppressive; neotropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vlnnerary; cardiant; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN MO2002102993-A2.
 XX PD 27-DEC-2002.
 XX PF 19-MAR-2002; 2002MO-US008123.
 XX PR 21-MAR-2001; 2001US-0277340P.
 XX PR 19-JUL-2001; 2001US-0306171P.
 XX PR 13-NOV-2001; 2001US-0331287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX WPI; 2003-175238/17.
 XX DR
 XX XX
 PT PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PT
 XX
 PS Claim 9; SEQ ID NO 322; 3205bp; English.
 XX
 XX The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences.
 CC
 CC Sequence 1892 BP; 461 A; 565 C; 472 G; 394 T; 0 U; 0 Other;
 CC
 CC Query Match 67.8%; Score 1284; DB 8; Length 1892;
 CC Best Local Similarity 99.7%; Pred. No. 0;
 CC Matches 1794; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

Qy	33	CGGATCTTCTCCGGCCATGAGAAAGCCAGCGCTGCTCTTCCCTCACTCTGAAGT	92
Db	22	CGGATCTTCTCCGGCCATGAGAAAGCCAGCGCTGCTCTTCCCTCACTCTGAAGT	81
Qy	93	GCTGCTCTGCTCTGCGACCTTCCGACGCTCCAGATTCACAGGCCCCCACTCCAG	152
Db	82	GCTGCTCTGCTCTGCGACCTTCCGACGCTCCAGATTCACAGGCCCCCACTCCAG	141
Qy	153	CAGCCCTCTCTCCCTAAGCAATGAGAGCTTCTGCACTGCTGCTCAACTGGA	212
Db	142	CAGCCCTCTCTCTCCCTAAGCAATGAGAGCTTCTGCACTGCTGCTCAACTGGA	201
Qy	213	GGCAGAGACTACCTGCGCTCTCCGTGCAACCCAGCGTCCGGAATCCACACTGTC	272
Db	202	GGCAGAGACTACCTGCGCTCTCCGTGCAACCCAGCGTCCGGAATCCACACTGTC	261
Qy	273	GCTGGAACCAATATGAAAAACAGGCTTATGTCCTGCTGCTGCTGCTGCTGCTG	332
Db	262	GCTGGAACCAATATGAAAAACAGGCTTATGTCCTGCTGCTGCTGCTGCTGCTG	321
Qy	333	TTATGCTCTCTGCTTGAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	392
Db	322	TTATGCTCTCTGCTTGAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	381
Qy	393	CTACTATGCAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	452
Db	382	CTACTATGCAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	441
Qy	453	CAAGAGATTAAGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	512
Db	442	CAAGAGATTAAGAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	501
Qy	513	CCACTTCAAGTACAGAAAGCCAGACCTTCCAGCTTCCAGCTTCCAGAGCTCAG	572
Db	502	CCACTTCAAGTACAGAAAGCCAGACCTTCCAGCTTCCAGAGCTTCCAGAGCTCAG	561
Qy	573	CGTGAAGAGCTCTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	632
Db	562	CGTGAAGAGCTCTCAATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	621
Qy	633	CAAGCAGAGCAAGAGTGGAGCAGAGCAGAGCCGACACAAAGACAAAGAGAGAG	692
Db	622	CAAGCAGAGCAAGAGTGGAGCAGAGCAGAGCCGACACAAAGACAAAGAGAGAG	681
Qy	693	GGGCGCAAAACAGAAAGAGCAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAG	752
Db	682	GGGCGCAAAACAGAAAGAGCAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAG	741
Qy	753	ACAGGGGACAAAG	812
Db	742	ACAGGGGACAAAG	801
Qy	813	GTTTCACTGATCTCTATCTTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT	872
Db	802	GTTTCACTGATCTCTATCTTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT	861
Qy	873	AGAGTCTACTCTATATATATGAGAAATCCAGAGCTCATTCAGTCCAGAGAAAT	932
Db	862	AGAGTCTACTCTATATATATGAGAAATCCAGAGCTCATTCAGTCCAGAGAAAT	921
Qy	933	AGATGAATGAATGAATATATATGAGAAATCTCTCTGAGAAACCAAAACCTGGCAG	992
Db	922	AGATGAATGAATGAATATATATGAGAAATCTCTCTGAGAAACCAAAACCTGGCAG	981
Qy	993	CTTCTGAGAGCTCCCAACAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1052
Db	982	CTTCTGAGAGCTCCCAACAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG	1040
Qy	1053	TACCTGATCATTAACCCCAAGCCCAAGGCTTGAAGTACATGAGAGAGAGATCTTGG	1112
Db	1041	TACCTGATCATTAACCCCAAGCCCAAGGCTTGAAGTACATGAGAGAGAGATCTTGG	1100

QY	1113	TTTCGGGAAGTGGCTGTGTGACAGCCTTGGGCGGCAACATCTCTACCTGTGGCCCTCTG	1172
Db	1101	TTTCGGGAAGTGGCTGTGTGACACCTTTGGCGGCAACATGTCTACCTGTGGCCCTCTG	1160
QY	1173	TGACTTCTGGCTCTTTGAAAGCTGGAGCAGTGCACCTCAGAGGCGAGCTGTGCAGCGGCAACA	1232
Db	1161	TGACTTCTGGCTCTTTGAAAGCTGGAGCAGTGCACCTCAGAGGCGAGCCTGTGAGCGGCAACA	1220
QY	1233	ATGGCAACCTCCCAAGAATCCCTCTTGTACAGCCCTCTGTGGCTCTCCAGAGCTGTCTC	1292
Db	1221	ATGGCAACCTCCCAAGAATCCCTTGTG-CAGCCCTTGTGTGCTCCAGAGCTGTCTC	1279
QY	1293	CATCGGCAACAGGTAGGGTCCCCAATAACAGCGGCTTTTACGGGCTGATTTGTATCAGG	1352
Db	1280	CATCGGCAACAGGTAGGGTCCCCAATAACAGCGGCTTTTACGGGCTGATTTGTATCAGG	1339
QY	1353	TGGGCTCCCATGATGACTTGTGTGTGTCGCCGCTTGCACAGAAAGGCTGTAAATATGTCCG	1412
Db	1340	TGGGCTCCCATGATGACTTGTGTGTGTCGCCGCTTGCACAGAAAGGCTGTAAATATGTCCG	1399
QY	1413	AGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAAGTTCAGAGATGGGATTTTCCCTACAA	1472
Db	1400	AGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAAGTTCAGAGATGGGATTTTCCCTACAA	1458
QY	1473	GATTGTGACACAGACTATATCCAGTACCCAACTACTGTTCCTTCAAAAAGCAGAGAGT	1532
Db	1459	GATTGTGACACAGACTATATCCAGTACCCAACTACTGTTCCTTCAAAAAGCAGAGAGT	1518
QY	1533	TCTGATGAGAAACCGCAATCGGAAGGTGTCCCGATGATGTCTCCAGATGAGACTTAA	1592
Db	1519	TCTGATGAGAAACCGCAATCGGAAGGTGTCCCGATGATGTCTCCAGATGAGACTTAA	1578
QY	1593	CAGTCCGCTGAGCCCTGGCAAAATGTGACAGCTGTGTCTTCATGTAGGACAGAGATTCAG	1652
Db	1579	CAGTCCGCTGAGCCCTGGCAAAATGTGACAGCTGTGTCTTCATGTAGGACAGAGATTCAG	1638
QY	1653	CACCTTGACTCTAAGCCAGATTCCGATAGCTGCGCTCTATTCTGTGCCACACCCCAAGCCA	1712
Db	1639	CACCTTGACTCTAAGCCAGATTCCGATAGCTGCGCTCTATTCTGTGCCACACCCCAAGCCA	1698
QY	1713	ACCTGCCCAAGTTCTCTAATGTTTTGAGACCCCATTTGCTTCAAGGCTGCCCTCTGGGT	1772
Db	1699	ACCTGCCCAAGTTCTCTAATGTTTTGAGACCCCATTTGCTTCAAGGCTGCCCTCTGGGT	1765
QY	1773	CTGTATTCTGGGCCCCCTACTACATTTCTTGGGTTGAGCAACAGTCCCAAGAGGGCCA	1832
Db	1759	CTGTATTCTGGGCCCCCTACTACATTTCTTGGGTTGAGCAACAGTCCCAAGAGGGCCA	1818

XX	08-MAY-2003.
PD	
XX	
PF	19-MAR-2002; 2002WO-US008277.
XX	
PR	21-MAR-2001; 2001US-0277340P.
PR	19-JUL-2001; 2001US-0306171P.
PR	13-NOV-2001; 2001US-0331287P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Rosen CA, Ruben SM;
XX	
DR	WPI; 2003-430516/40.
DR	P-PSDB; ADC74193.
XX	
PT	New human secreted polypeptide for diagnosing, preventing or treating
PT	hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT	disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
XX	atherosclerosis).
XX	
PS	Claim 27; SEQ ID NO 211; 2272pp; English.
XX	

Query Match	67.8%;	Score 1284;	DB 10;	Length 1892;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 1794;	Conservative	0;	Mismatches 3;	Indels 1

[illegible]

Db 697 GTTACTATCCAGAGAGTCTGTGTCCAGCACTCTCTATCTCTACTAAGACT 756
Qy 451 CTCAGAGATAGAGCTTCAGCTGAAGTCTCAACCAAGATGACTCCCATCTCA 510
Db 757 CTGAAGAGATAGAGCTTCAGCTGAAGTCTCAACCAAGATGACTCCCATCTCA 816
Qy 511 CCCCACTTCACAGTACAGAACCCAGACCTTCCAGCTTGGCTGGAGAGCTTCA 570
Db 817 CCCCACTTCACAGTACAGAACCCAGACCTTCCAGCTTGGCTGGAGAGCTTCA 876
Qy 571 AAGTGAAGAGCTCTCAACATCTCTCTTGTCTGGAGAGCCAGAGAGAGCCAG 630
Db 877 AAGTGAAGAGCTCTCAACATCTCTCTTGTCTGGAGAGCCAGAGAGAGCCAG 936
Qy 631 CACAAGCAGAGAGAGAGTGAAGCAGAGAGAGAGCCAGCACAAGAGAGAGAG 690
Db 937 CACAAGCAGAGAGAGAGTGAAGCAGAGAGAGAGCCAGCACAAGAGAGAGAG 996
Qy 691 GAGGGGAG 750
Db 997 GAGGGGAG 1056
Qy 751 GAG 810
Db 1057 GAG 1116
Qy 811 AAGTTCACTCTGAATCTCTATCTCTTCAACCTTCTCTTGTCTGGAGAGAG 870
Db 1117 AAGTTCACTCTGAATCTCTATCTCTTCAACCTTCTCTTGTCTGGAGAGAG 1176
Qy 871 GTAGAGCTTACTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
Db 1177 GTAGAGCTTACTCTATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
Qy 931 ATAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA 990
Db 1237 ATAGATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1296
Qy 991 AGCTTCTGAGCTGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
Db 1297 AGCTTCTGAGCTGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1356
Qy 1051 AATACCTGATCATTAACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
Db 1357 AATACCTGATCATTAACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
Qy 1111 GGTTCGGAG 1170
Db 1417 GGTTCGGAG 1476
Qy 1171 TGTGACTTCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
Db 1477 TGTGACTTCTGCTCTTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1536
Qy 1231 CAATGAGACACTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1290
Db 1537 CAATGAGACACTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596
Qy 1291 TCATGAGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1350
Db 1597 TCATGAGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1656
Qy 1351 GGTGGGCTCCAGATG 1365
Db 1657 GGTGGGCTCCAGATG 1671

RESULT 11
ID ADO24565
AC ADO24565 standard; cDNA; 3306 BP.
XX ADO24565;
XX

DT 12-AUG-2004 (first entry)
XX
DE Human PRO7347 encoding cDNA SEQ ID NO:204.
XX
KW human; PRO; antiaemic; antirheumatic; antineoplastic; antiparasitic;
KW antineoplastic; dermatological; immunostimulant; immunosuppressive;
KW osteopathic; vasotropic; immune response; rheumatoid arthritis;
KW juvenile chronic arthritis; systemic lupus erythematosus;
KW spondyloarthritis; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
KW splenomegaly; leukopenia; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004043397-A2.
XX
PD 27-MAY-2004.
XX
PF 12-NOV-2003; 2003MO-US036002.
XX
PR 12-NOV-2002; 2002US-0425931P.
XX
PA (GENTH) GENENTECH INC.
PI Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;
XX
XX WPI; 2004-420080/39.
DR P-FSDB; ADO24566.
XX
PT New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,
PT capable of stimulating an immune response, useful for treating diseases
PT such as rheumatoid arthritis, psoriasis, and leukopenia.
XX
PS Claim 2; SEQ ID NO 204; 326pp; English.
XX
CC The present invention describes an isolated human PRO polypeptide (I).
CC Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a
CC vector (III) comprising (II); (3) a host cell (IV) comprising (III); (4)
CC producing (I); (5) a chimeric molecule (V) comprising (I) fused to a
CC heterologous amino acid sequence; (6) an antibody (VI) which specifically
CC binds to (I); (7) a composition of matter comprising (I), an agonist of
CC (I), an antagonist of (I), or (VI) in combination with a carrier; (8)
CC treating (M1) an immune related disorder in a mammal, by administering
CC (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)
CC diagnosing an immune related disease in a mammal, by detecting the level
CC of expression of a gene encoding (I) in a test sample of tissue cells
CC obtained from the mammal and in a control sample of known normal tissue
CC cells of the same cell type; (10) identifying a compound that inhibits
CC the activity of (I); (11) identifying a compound (M2) that inhibits the
CC expression of a gene encoding (I); (12) identifying a compound that
CC mimics the activity of (I); and (12) stimulating the immune response in a
CC mammal, by administering (I) or its antagonist to the mammal. (I) has
CC antineoplastic, antirheumatic, antineoplastic, antiparasitic,
CC antineoplastic, dermatological, immunostimulant, immunosuppressive,
CC osteopathic and vasotropic activities. (I) and (VI) are useful for
CC diagnosing an immune related disease in a mammal. (II) is useful for
CC diagnosing an inflammatory immune response in a mammal. (VI) is useful
CC for determining the presence of (I) in a sample suspected of containing
CC the polypeptide. (M1) is useful for treating mammal having an immune
CC related disorder chosen from rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, systemic lupus erythematosus,
CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune or immune-mediated skin
CC diseases including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
CC present sequence encodes a human PRO protein from the present invention.
XX
SQ Sequence 3306 BP; 737 A; 950 C; 821 G; 746 T; 0 U; 52 Other;

Query Match 28.3%; Score 536; DB 12; Length 3306;
 Best Local Similarity 100.0%; Pred. No. 2.2e-247;
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1025 TGTGCTGTGCTATTCGATCGTGAAGAAATACCTGATCATATACCCCAAGCCCT 1084
 DB 1890 TGTGCTGTGCTATTCGATCGTGAAGAAATACCTGATCATATACCCCAAGCCCT 1949
 QY 1085 GGAATACATGAGAGAGAGATCTTGTGTTGCGAAAGTGGTCTGTGACAGCCCTTGAGC 1144
 DB 1950 GGAATACATGAGAGAGAGATCTTGTGTTGCGAAAGTGGTCTGTGACAGCCCTTGAGC 2009
 QY 1145 GGGACACATGTCTACCTGTGCTCTGTGATCTTGTGCTCTGTGAGAGCTGAGCTGCC 1204
 DB 2010 GGGACACATGTCTACCTGTGCTCTGTGATCTTGTGCTCTGTGAGAGCTGAGCTGCC 2069
 QY 1205 ACTGAGAGGCGAGCGCTGCAAGCGGCAACATGCGACACTTCCCAAGAGCTCCCTTTGTCA 1264
 DB 2070 ACTGAGAGGCGAGCGCTGCAAGCGGCAACATGCGACACTTCCCAAGAGCTCCCTTTGTCA 2129
 QY 1265 GCGCTTGTGCTGCTCCAGAGCTGTGCTGATCGGCAACAGAGTGGTCCCAAGATCAG 1324
 DB 2130 GCGCTTGTGCTGCTCCAGAGCTGTGCTGATCGGCAACAGAGTGGTCCCAAGATCAG 2189
 QY 1325 GCGCTTGTGCTGCTGCTGATGTTGTACGTGGGCTCCACATGAGACTTGTGCTGCGCGC 1384
 DB 2190 GCGCTTGTGCTGCTGCTGATGTTGTACGTGGGCTCCACATGAGACTTGTGCTGCGCGC 2249
 QY 1385 TTGCGACGAAAGGCTGTGAAGATGTCCGAGTCTGCGGCTGCTCCAGCTGATCTCTTA 1444
 DB 2250 TTGCGACGAAAGGCTGTGAAGATGTCCGAGTCTGCGGCTGCTCCAGCTGATCTCTTA 2309
 QY 1445 GCTTCAGAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCAG 1504
 DB 2310 GCTTCAGAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCAG 2369
 QY 1505 ACTACTGTCTCTTCAAAAGCGAGCTGTGATGAGAAACCGCAATCGAAGGTG 1560
 DB 2370 ACTACTGTCTCTTCAAAAGCGAGCTGTGATGAGAAACCGCAATCGAAGGTG 2425

RESULT 12

AAK97739 standard; DNA; 964 BP.
 AAK97739;

13-SEP-1999 (first entry)

Extended human secreted protein coding sequence, SEQ ID NO. 304.

Secretd protein; human; cytokine; cellular proliferation; cell movement;
 cellular differentiation; immune system regulator; anti-inflammatory;
 haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
 reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 genetic disease; sr.

Homo sapiens.

W09931236-A2.

24-JUN-1999.

17-DEC-1998; 98MO-IB002122.

17-DEC-1997; 97US-0069957P.

09-FEB-1998; 98US-0074121P.

13-APR-1998; 98US-0081563P.

10-AUG-1998; 98US-0096116P.

(BEST) GENSET.

PI Bouquelieret L, Duclert A, Dumas Milne Edwards J;
 XX WPI, 1999-385906/32.
 DR P-PSDB; AAY36055.

New isolated human secreted proteins.

Claim 1; Page 377; 516pp; English.

This sequence represents an extended human secreted protein coding
 sequence of the invention. The secreted proteins can be used in treating
 or controlling a variety of human conditions. The secreted proteins may
 act as cytokines or may affect cellular proliferation or differentiation
 or may act as immune system regulators, haematopoiesis regulators, tissue
 growth regulators, regulators of reproductive hormones or cell movement
 or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
 tumour inhibition activity. The DNAs can be used in forensic procedures
 to identify individuals or in diagnostic procedures to identify
 individuals having genetic diseases resulting from abnormal expression of
 the genes corresponding to the extended cDNAs. They are also useful for
 constructing a high resolution map of the human chromosomes. They can
 also be used for gene therapy to control or treat genetic diseases

Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;

Query Match 27.9%; Score 528; DB 2; Length 964;
 Best Local Similarity 99.3%; Pred. No. 1.6e-243;
 Matches 948; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 30 GGGCGGATCTTCTCCGCGCATGAGAGCGCGCTGCTCTCTCTCACTCTGAA 89
 DB 2 GGGCGGATCTTCTCCGCGCATGAGAGCGCGCTGCTCTCTCTCTCACTCTGAA 61
 QY 90 GGTGTGCTCTGCTCTGCGACCTGCGCGCGCGCGAGATTCAGTCAAGGCCCCCACTCC 149
 DB 62 GGTGTGCTCTGCTCTGCGACCTGCGCGCGCGCGAGATTCAGTCAAGGCCCCCACTCC 121
 QY 150 AGGCGCCCTCTCTCTCTCCATGCAATGCAACGCTTGTGCACTGCTCAACTG 209
 DB 122 AGGCGCCCTCTCTCTCTCCATGCAATGCAACGCTTGTGCACTGCTCAACTG 181
 QY 210 GAAGCGAGACTACTGCGCTCTCGGTGCAACCGAGTGGCGGATTCGCACTGCT 269
 DB 182 GAAGCGAGACTACTGCGCTCTCGGTGCAACCGAGTGGCGGATTCGCACTGCT 241
 QY 270 CCACTGAGACCAATATGAAACCAACGCTTATGCGCGATGCTGTCTGCAACT 329
 DB 242 CCACTGAGACCAATATGAAACCAACGCTTATGCGCGATGCTGTCTGCAACT 301
 QY 330 CCTTATGCTCTGCTGCTTGTGAGCTTCTGCGAGTCACTCACTGCTGCAACA 389
 DB 302 CCTTATGCTCTGCTGCTTGTGAGCTTCTGCGAGTCACTCACTGCTGCAACA 361
 QY 390 CGTCTACTATGCGAAGAGTCTGTTTCCAGCGAGTCTATCTCTCACTCAAC 449
 DB 362 CGTCTACTATGCGAAGAGTCTGTTTCCAGCGAGTCTATCTCTCTCTCAAC 421
 QY 450 TCTCAAGAGATGAGCTTCACTGAGTCAACCCACAC-GATGACTCTCCCATCT 508
 DB 422 TCTCAAGAGATGAGCTTCACTGAGTCAACCCACAC-GATGACTCTCCCATCT 481
 QY 509 CACCCCACTTCAAGTGAAGAGCCGAGCTTCCAGCCCTGCGCTGAGAGGCTTCA 568
 DB 482 CACCCCACTTCAAGTGAAGAGCCGAGCTTCCAGCCCTGCGCTGAGAGGCTTCA 541
 QY 569 ACAAGTGAAGAGCTCCCTACCAATCTCTGCTGCTGAGAGGCTGAGAGGCTGAG 628
 DB 542 ACAAGTGAAGAGCTCCCTACCAATCTCTGCTGCTGAGAGGCTGAGAGGCTGAG 601
 QY 629 AGCAAGAGAGAGAGAGTGAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 688
 DB 602 AGCAAGAGAGAGAGAGTGAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 661

QY 689 AAGAGGGGCGAGAAACAGAGAGCAAGAGAAACAGAGAGAGAGAGAGAG 748
DB 662 AAGAGGGGCGAGAAACAGAGAGCAAGAGAGAAACAGAGAGAGAGAGAG 721
QY 749 AAG 808
DB 722 AAG 781
QY 809 CCAAGTTTCACTGTAATCTCTATCTTAAACCTTCTCTTTTGTCTCCCGGGTACGAG 868
DB 782 CCAAGTTTCACTGTAATCTCTATCTTAAACCTTCTCTTTTGTCTCCCGGGTACGAG 841
QY 869 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 928
DB 842 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 901
QY 929 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 983
DB 902 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 956

RESULT 13

ADP19006 standard; cDNA; 964 BP.

ADP19006;

26-AUG-2004 (first entry)

Human secreted polynucleotide #262.

Human; secreted protein; gene; ss; genetic disease.

Homo sapiens.

US004110939-A1.

10-JUN-2004.

15-OCT-2001; 2001US-00978360.

17-DEC-1998; 98MO-1B002122.

09-FEB-1999; 99MO-1B000282.

21-JUN-2000; 2000MO-1B000951.

15-SEP-2000; 2000US-00663600.

(GEST) GENSET SA.

Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;

Duclet A;

MPI; 2004-440404/41.

P-PSDB; ADP19411.

New isolated polynucleotide encoding secreted polypeptide, useful for

gene therapy, or in diagnostic procedures to identify individuals having

genetic diseases resulting from abnormal expression of the genes.

Claim 1; SEQ ID NO 262; 113bp; English.

The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polynucleotides are useful for expressing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do or do not express the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polynucleotide of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.

SQ Sequence 964 BP; 258 A; 294 C; 227 G; 180 T; 0 U; 5 Other;

Query Match 27.9%; Score 528; DB 12; Length 964;

Best Local Similarity 99.3%; Pred. No. 1.6e-243;

Matches 948; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 30 GGGGGATCTTCTCCGCGCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 89
DB 2 GGGGGATCTTCTCCGCGCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 61
QY 90 GGTGCTCTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 149
DB 62 GGTGCTCTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
QY 150 AGGAG 209
DB 122 AGGAG 181
QY 210 GAG 269
DB 182 GAG 241
QY 270 CAG 329
DB 242 CAG 301
QY 330 CCGTTATGCTCTGCTGTTGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 389
DB 302 CCGTTATGCTCTGCTGTTGAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 361
QY 390 GGTCTACTAGCAAG 449
DB 362 GGTCTACTAGCAAG 421
QY 450 TCTCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
DB 422 TCTCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481
QY 509 CACCCCACTTCAAG 568
DB 482 CACCCCACTTCAAG 541
QY 569 ACAAGGTGAG 628
DB 542 ACAAGGTGAG 601
QY 629 AGCACAAG 688
DB 602 AGCACAAG 661
QY 689 AAGAGGGGCGAGAAACAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
DB 662 AAGAGGGGCGAGAAACAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
QY 749 AAG 808
DB 722 AAG 781
QY 809 CCAAGTTTCACTGTAATCTCTATCTTAAACCTTCTCTTTTGTCTCCCGGGTACGAG 868
DB 782 CCAAGTTTCACTGTAATCTCTATCTTAAACCTTCTCTTTTGTCTCCCGGGTACGAG 841
QY 869 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 928
DB 842 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 901
QY 929 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 983
DB 902 AAGTAGAGTCTACTCTATGATTAAGAGAAATCAGAGAGCTCATTCGATCAGCCAGG 956

Query Match 17.9%; Score 339; DB 8; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.8e-152;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1557	GGTGTCCCGCATATGATGTCTGCAAGATGAGACTTACAGTGGCGTGAAGCCCTGGCAAAAG	1616
DB	177	GGTGTCCCGCATGAGATGCTGCAAGATGAGACTTACAGTGGCGTGAAGCCCTGGCAAAAG	236
QY	1617	TGAGACGTTGCTGCTGATGAGACCGAGAGTTGAGCACCCTTGACTAGAGCCAGTTGG	1676
DB	237	TGAGACGTTGCTGCTGATGAGACCGAGAGTTGAGCACCCTTGACTAGAGCCAGTTGG	296
QY	1677	ATGAGCTGGCGGTCTATTCTGCCCCACACCCAGCCCACTGCCCCAGTTCTATTGTTT	1736
DB	297	ATGAGCTGGCGGTCTATTCTGCCCCACACCCAGCCCACTGCCCCAGTTCTATTGTTT	356
QY	1737	TGAGACCCCTTGTCTTCAAGGCTGCCCTTCTGGGTCTGTTACTGGGCCCTTACTCAGAT	1796
DB	357	TGAGACCCCTTGTCTTCAAGGCTGCCCTTCTGGGTCTGTTACTGGGCCCTTACTCAGAT	416
QY	1797	TTCCTTGGGTTTGAGCAACAGTCCCAAGAGAGGCGCACGTTGGAGCTGGCCCTTAA	1856
DB	417	TTCCTTGGGTTTGAGCAACAGTCCCAAGAGAGGCGCACGTTGGAGCTGGCCCTTAA	476
QY	1857	AAGATGACTTTACATAAAATGTTGATCTTCAAAAAAAA	1895
DB	477	AAGATGACTTTACATAAAATGTTGATCTTCAAAAAAAA	515

Search completed: March 7, 2005, 23:21:24
Job time : 1125 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 15:17:16 ; Search time 1099 Seconds
(without alignments)
10231.701 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895

Sequence: 1 gttagaggcggtgtgtcc.....tgttgatcttcaaaaaaa 1895

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1895	100.0	1895	17	US-10-148-641A-23
2	1886	99.5	1886	16	US-10-262-666-41
3	1886	99.5	1886	17	US-10-085-117-53
4	1881.8	99.3	1892	18	US-10-719-993-124
5	1856.4	98.0	1899	10	US-09-748-783-77
6	1811.2	95.6	1892	10	US-09-397-945-90
7	1811.2	95.6	1892	17	US-10-653-595-90
8	1632	86.1	1632	17	US-10-085-117-54
9	1271.8	67.1	1671	17	US-10-296-115-693
10	1128.2	59.5	1840	17	US-10-085-117-50
11	1062.6	56.1	1623	17	US-10-085-117-51
12					Sequence 23, Appl
13					Sequence 41, Appl
14					Sequence 53, Appl
15					Sequence 124, Appl
16					Sequence 77, Appl
17					Sequence 90, Appl
18					Sequence 54, Appl
19					Sequence 693, Appl
20					Sequence 50, Appl
21					Sequence 51, Appl

12	937.6	49.5	964	11	US-09-978-360A-262	Sequence 262, App
13	471.8	24.9	21347	18	US-10-719-993-6794	Sequence 6794, Ap
14	471.8	24.9	29346	17	US-10-085-117-52	Sequence 52, Appl
15	433.8	22.9	469	10	US-09-918-995-14842	Sequence 14842, A
16	408.4	21.6	474	10	US-09-918-995-36471	Sequence 36471, A
17	337.2	17.8	522	18	US-10-474-495-12	Sequence 12, Appl
18	332	17.5	28953	18	US-10-719-993-6811	Sequence 6811, Ap
19	329.8	17.4	507	18	US-10-474-495-230	Sequence 230, App
20	328	17.3	24923	18	US-10-719-993-7043	Sequence 7043, Ap
21	282.4	14.9	308	13	US-10-040-739-641	Sequence 641, App
22	275.8	14.6	36211	17	US-10-085-117-49	Sequence 49, Appl
23	200.6	10.6	201	18	US-10-719-993-2295	Sequence 2295, Ap
24	200.6	10.6	201	18	US-10-719-993-2296	Sequence 2296, Ap
25	199	10.5	201	18	US-10-719-993-2297	Sequence 2297, Ap
26	199	10.5	201	18	US-10-719-993-2298	Sequence 2298, Ap
27	154.6	8.2	157	18	US-10-719-993-2299	Sequence 2299, Ap
28	154.6	8.2	201	18	US-10-719-993-15249	Sequence 15249, A
29	154.6	8.2	201	18	US-10-719-993-17827	Sequence 17827, A
30	139.8	7.4	201	18	US-10-719-993-15240	Sequence 15240, A
31	135.4	7.1	201	18	US-10-719-993-15253	Sequence 15253, A
32	126.6	6.7	370	9	US-09-728-445-80	Sequence 80, Appl
33	119.6	6.3	201	18	US-10-719-993-15250	Sequence 15250, A
34	110.6	5.8	201	18	US-10-719-993-15236	Sequence 15236, A
35	95.4	5.0	201	18	US-10-719-993-15238	Sequence 15238, A
36	88.4	4.7	201	18	US-10-719-993-15251	Sequence 15251, A
37	88	4.6	201	18	US-10-719-993-15239	Sequence 15239, A
38	75.6	4.0	28796	13	US-10-087-182-1297	Sequence 1297, Ap
39	74	3.9	628	16	US-10-029-386-22859	Sequence 22859, A
40	73.4	3.9	51259	17	US-10-374-077-209	Sequence 209, App
41	72.6	3.8	16442	17	US-10-374-077-208	Sequence 208, App
42	71.2	3.8	1926	15	US-10-294-804-3	Sequence 3, Appli
43	71.2	3.8	1926	18	US-10-194-046-3	Sequence 3, Appli
44	71.2	3.8	8705	15	US-10-291-230-14	Sequence 14, Appl
45	71.2	3.8	8705	15	US-10-291-249-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-148-641A-23
; Sequence 23, Application US/10148641A
; Publication No. US20040086852A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Toshio and Nakayama, Eiichi
; TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES
; FILE REFERENCE: L00461.70132 US
; CURRENT APPLICATION NUMBER: US/10/148,641A
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/559,013
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/168,353
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49) ... (1677)
US-10-148-641A-23

Query Match 100.0%; Score 1895; DB 17; Length 1895;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGAGCGGCTTGTGTCCACGGACGCGGCGGATCTTCTCCGCCATGAGGAAGCCA 60
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Db 1 GTTAGAGCGGCTTGTGTCCACGGACGCGGCGGATCTTCTCCGCCATGAGGAAGCCA 60
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 1886
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (49)..(1680)
OTHER INFORMATION:
US-10-262-666-41

Query Match 99.5%; Score 1886; DB 16; Length 1886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTATGAGGCGGCTTGTGTCCACGGGACGGGGCGGATCTTCTCCGGCCATGAGGAAGCCA	60
DB	1	GTATGAGGCGGCTTGTGTCCACGGGACGGGGCGGATCTTCTCCGGCCATGAGGAAGCCA	60
QY	61	GCGCTGGCTTCTTCCCTCACTCCCTGAAAGTCTCTCTCTGCTCTGACACCTGCCGA	120
DB	61	GCGCTGGCTTCTTCCCTCACTCCCTGAAAGTCTCTCTCTGCTCTGACACCTGCCGA	120
QY	121	GCCAGGATTCGACTCAGGCCCCCACTCCAGGAGGCGCTCTCTCTCTACCGAATACGAA	180
DB	121	GCCAGGATTCGACTCAGGCCCCCACTCCAGGAGGCGCTCTCTCTCTACCGAATACGAA	180
QY	181	CGCTTCTTCCGACTGCTGACTCAACTGGAAGGAGAGACTACTGCGCGTCTCCGTGCA	240
DB	181	CGCTTCTTCCGACTGCTGACTCAACTGGAAGGAGAGACTACTGCGCGTCTCCGTGCA	240
QY	241	ACCAGGCTGCCGGAATCCCACTCCCTGAGTCCAGTCCCAATATGAAACCAACCGCTTA	300
DB	241	ACCAGGCTGCCGGAATCCCACTCCCTGAGTCCAGTCCCAATATGAAACCAACCGCTTA	300
QY	301	GTGCCGATGGTGTCTGTCTCTCAACTCCCTTATGCTCTCTGCTTGTGAGTCTTCTGC	360
DB	301	GTGCCGATGGTGTCTGTCTCTCAACTCCCTTATGCTCTCTGCTTGTGAGTCTTCTGC	360
QY	361	CAGTTCACTACCTACCGTGTCTCAACAGTCTACTATGCAAGAGAGTCTGTGTTC	420
DB	361	CAGTTCACTACCTACCGTGTCTCAACAGTCTACTATGCAAGAGAGTCTGTGTTC	420
QY	421	CAGCCAGTCTCTATCTCTCACTCACTCTCAAGGATAGAGCTTCACTGAGTCA	480
DB	421	CAGCCAGTCTCTATCTCTCACTCACTCTCAAGGATAGAGCTTCACTGAGTCA	480
QY	481	TCACCCACCAAGTACCTCCCTCACTCTCAAGGATAGAGCTTCACTGAGTCA	540
DB	481	TCACCCACCAAGTACCTCCCTCACTCTCAAGGATAGAGCTTCACTGAGTCA	540
QY	541	TTCCAGCCCTGGCTGAGAGGCTCAGCAACAACTGGAAGAGTCTCTCAATCTCTCTG	600
DB	541	TTCCAGCCCTGGCTGAGAGGCTCAGCAACAACTGGAAGAGTCTCTCAATCTCTCTG	600
QY	601	TCCCTGGAGGCGCAGGAGCAAGCCGACAGCAACAGCAGGAGGAGTGGAGCAGG	660
DB	601	TCCCTGGAGGCGCAGGAGCAAGCCGACAGCAACAGCAGGAGGAGTGGAGCAGG	660
QY	661	CAGGAGCGCACAAGAACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
DB	661	CAGGAGCGCACAAGAACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	720
QY	721	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
DB	721	GAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	780
QY	781	GTGTCTCAGTCCAGCAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTAAC	840
DB	781	GTGTCTCAGTCCAGCAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTAAC	840
QY	841	CCTTCTCTTTTGTCTCCCGGCTACGAGAGTAGAGTCTACTCTATGATATGAGAAC	900
DB			

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US-10-085-117-53


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QY 1861 TGACTTTACATAAAATGTTGATCTTC 1886
Db 1861 TGACTTTACATAAAATGTTGATCTTC 1886

RESULT 4
US-10-719-993-124
; Sequence 124, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 5342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-124

Query Match 99.3%; Score 1881.8; DB 18; Length 1892;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1880; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGAGGGCGCTGTGTCCACGGGACGGGGCGGATCTTCCGGCCCATGAGGAAGCCA 60
Db 4 GTTAGAGGGCGCTGTGTCCACGGGACGGGGCGGATCTTCCGGCCCATGAGGAAGCCA 63

QY 61 GCGCTGGCTTCTTCCCTCACTCTCGAAGGTGTCTGCTGCTGCTGGCACTGCGCA 120
Db 64 GCGCTGGCTTCTTCCCTCACTCTCGAAGGTGTCTGCTGCTGCGCACTGCGCA 123

QY 121 GCCCAGGATTCGACTCAGCGCCCACTCCAGGCGCCCTCTCTCTCTACCGAATACGAA 180
Db 124 GCCCAGGATTCGACTCAGCGCCCTCACTCCAGGCGCCCTCTCTCTCTACCGAATACGAA 183

QY 181 CGCTTCTTCGCACTGTGACTCCAACTCGAAGGCGAGACTACCTGCGGTCTCCGTGCA 240
Db 184 CGCTTCTTCGCACTGTGACTCCAACTCGAAGGCGAGACTACCTGCGGTCTCCGTGCA 243

QY 241 ACCCAGGTGCGGAATCCCACTCTGCTCCAGCTGGACCAATATGAAACCAACGGCTTA 300
Db 244 ACCCAGGTGCGGAATCCCACTCTGCTCCAGCTGGACCAATATGAAACCAACGGCTTA 303

QY 301 GTGCCCGATGGTGTCTGCTCTCAACCTCCCTTATGCTCTGCTTGTGAGTCTTCTGC 360
Db 304 GTGCCCGATGGTGTCTGCTCTCAACCTCCCTTATGCTCTGCTTGTGAGTCTTCTGC 363

QY 361 CAGTTTCACCTACCTACCTGCTCCAACTGCTCTATGCTCCAAAGAGAGTCTGCTGCTCC 420
Db 364 CAGTTTCACCTACCTACCTGCTCCAACTGCTCTATGCTCCAAAGAGAGTCTGCTGCTCC 423

QY 421 CAGCCAGTCTTATCTCTCACTAACTCTCAAGGAGATGAAGCTTCAGCTGAAGTC 480
Db 424 CAGCCAGTCTTATCTCTCACTAACTCTCAAGGAGATGAAGCTTCAGCTGAAGTC 483

QY 481 TCACCCACCAAGATGATCTCCCATCTCACCCTCACTTCAAGTGAAGAGCCGACGAC 540
Db 484 TCACCCACCAAGATGATCTCCCATCTCACCCTCACTTCAAGTGAAGAGCCGACGAC 543

QY 541 TTCCAGCCCTGCTGAGAGGCTCAGCAACAGCTGGAGAGCTCTCAATCTCTCTTG 600
Db 544 TTCCAGCCCTGCTGAGAGGCTCAGCAACAGCTGGAGAGCTCTCAATCTCTCTTG 603

QY 601 TCCCTGGAGGCGCAGGAGCAAGCGCCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGG 660
Db 604 TCCCTGGAGGCGCAGGAGCAAGCGCCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAGG 663
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Qy 1267 CCCTTCTTGCCTCCAGAGCTGTCCATCGGCAACAGTAGGTGCTCCAGAAATCAGGC 1326
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Qy 1327 CGCTTTTACGGCTGGATTGTACGGTGGCTCCACATGAGACTTCTGGTGTGCGCGCTT 1386
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Qy 1447 TTCCAGATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAAAC 1506
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Qy 1507 TACTGTTCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGC 1566
Db 1501 TACTGTTCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGC 1560
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Qy 1627 GTGC-TTCATGAGCCAGGATTCAGACCTTGACTCTAGGCCAGTTTCGGATGAGCTGG 1685
Db 1620 GTGCTTTCATGAGCCAGGATTCAGACCTTGACTCTAGGCCAGTTTCGGATGAGCTKG 1679
Qy 1686 CGTCTATTCTGCCACACCCAGCCCAACTGCCCCAGCTTCTCTATTGTTTGGAGACCCC 1745
Db 1680 SGTATTATTGCCCCACACCCAGCCCAACTGCCCCAGCTTCTCTATTGTTTGGAGACCCC 1739
Qy 1746 ATTGCTTTTCCAGCTGCCCTTCTGGGTCTGTGTTACTCGGCCCTTACTCAATTTCTTTGGG 1805
Db 1740 ATTGCTTTTCCAGCTGCCCTTCTGGGTCTGTGTTACTCGGCCCTTACTCAATTTCTTTGGG 1799
Qy 1806 TTGGAGCAACAGTCCAGAGAGGCCACCGTGGGAGCTGGCCCTCTTAAAGATGACT 1865
Db 1800 TTGGAGCAACAGTCCAGAGAGGCCACCGTGGGAGCTGGCCCTCTTAAAGATGACT 1859
Qy 1866 TTACATAAAATGTTGATCTTCAAAAAAAA 1895
Db 1860 TTACATAAAATGTTGATCTTCAAAAAAAA 1889

RESULT 6

US-09-397-945-90
; Sequence 90, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312

; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-945-90

Query Match 95.6%; Score 1811.2; DB 10; Length 1892;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
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Db 13 GGACGCGGAGGATCTTCTCCGCCCATGAGGAAGCCAGCGCTGGCTTCTTCCCTCACT 72
Qy 84 CTGAAGGTGCTGCTCTGCTCTGCACTTGGCACTTGGCCGAGCCGAGGATTCGATCAGGCCCC 143
Db 73 CTGAAGGTGCTGCTCTGCTCTGCACTTGGCACTTGGCCGAGCCGAGGATTCGATCAGGCCCC 132
Qy 144 CACTCCAGCAGCCCTCTCTCTACCAATACGAAGCTTCTTGGCACTGCTGATCC 203
Db 133 CACTCCAGCAGCCCTCTCTCTACCAATACGAAGCTTCTTGGCACTGCTGATCC 192
Qy 204 AACCTGGAAGGAGAGACTTACCTGCGTCTCGTGCACCAACCCAGCGTGCAGGAATCCAC 263
Db 193 AACCTGGAAGGAGAGACTTACCTGCGTCTCGTGCACCAACCCAGCGTGCAGGAATCCAC 252
Qy 264 ACTGTCAGCTGGACCAATATGAAAAACCAACCGCTTGTGCGGATGGTGTCTGTCTC 323
Db 253 ACTGTCAGCTGGACCAATATGAAAAACCAACCGCTTGTGCGGATGGTGTCTGTCTC 312
Qy 324 CAACTCTCCCTTATGCTCTGCTGTTGAGTCTTCTGCGAGTTCACTACCTACGTTGCTC 393
Db 313 CAACTCTCCCTTATGCTCTGCTGTTGAGTCTTCTGCGAGTTCACTACCTACGTTGCTC 372
Qy 384 CAACCACTCTACTATGCAAGAGAGTCTGTTGTTCCAGCCAGTCTCTATTCTCTCACC 443
Db 373 CAACCACTCTACTATGCAAGAGAGTCTGTTGTTCCAGCCAGTCTCTATTCTCTCACC 432
Qy 444 TAACACTCTCAAGGAGATAGAGCTTCACTGAAAGTCTCACCCACCAACGATGACTCCCC 503
Db 433 TAACACTCTCAAGGAGATAGAGCTTCACTGAAAGTCTCACCCACCAACGATGACTCCCC 492
Qy 504 CATCTCACCCACTTCAAGTACAGTACAGAGCCAGAGCTTCCAGCCCTGGCTGAGAGGCT 563
Db 493 CATCTCACCCACTTCAAGTACAGTACAGAGCCAGAGCTTCCAGCCCTGGCTGAGAGGCT 552
Qy 564 CAGCAACAACCTGGAAGAGTCTCTCAATCTCTTGTCTCCCTGGGAGGCCAGGAGCAAGC 623
Db 553 CAGCAACAACCTGGAAGAGTCTCTCAATCTCTTGTCTCCCTGGGAGGCCAGGAGCAAGC 612
Qy 624 GCCAGAGCACAAGCAGGAGCAAGGAGTGGAGCAGCAGGAGGAGCCGACACAAACACAA 683
Db 613 GCCAGAGCACAAGCAGGAGCAAGGAGTGGAGCAGCAGGAGGAGCCGACACAAACACAA 672
Qy 684 GCAGGAAGAGGGGAGAGAAACAGAGAGAGCAAGAGAGAAAGAGAGAGAGAGAGAGCA 743
Db 673 GCAGGAAGAGGGGAGAGAAACAGAGAGAGCAAGAGAGAAAGAGAGAGAGAGAGCA 732
Qy 744 GGAACAAGCAGAGGGGAGTAAAGGAGGAGGAGGCTGTGCTCAGCTGCAGCAGACTC 803

Db 733 GGAAGGACAGGGGACTAAGAGGAGCGGAGGCTGTGTCTCAGCTGCAGACACTC 792
QY 804 AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAACCCCTTCTCTTTTGTCTCCCGGGT 863
Db 793 AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAACCCCTTCTCTTTTGTCTCCCGGGT 852
QY 864 ACCAGAAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGAGCTCATTCGATCAGC 923
Db 853 ACCAGAAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGAGCTCATTCGATCAGC 912
QY 924 CMAGAAATAGATGAATGAATGAATATATGATGAGAACTCTTACTGAGAAACCAAA 983
Db 913 CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTTACTGAGAAACCAAA 972
QY 984 CCTGCGACCTCTCTGCGAGTCCGCCACACAGAGCCCTTGTGTGTGTCTATTTCGAT 1043
Db 973 CCTGCGACCTCTCTGCGAGTCCGCCACACAGA-GCCTTGTGTGTGTGTCTATTTCGAT 1031
QY 1044 COTGAGAAATACCTGCATCATAACCCACAGCCCAAGCCCTGGAAGTACATGAGGAGGA 1103
Db 1032 COTGAGAAATACCTGCATCATAACCCACAGCCCAAGCCCTGGAAGTACATGAGGAGGA 1091
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QY 1224 GCGGCAACAATGCGACACCTCCCAAGACTTCTTGTGTGAGCCCTTGTCTTCCCTCCCA 1283
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Db 1271 GAGCTGTGCTCATCGGCAACAGGTAGGCTCCCAAGATCAGGCGGCTTTTACGGGTGGA 1330
QY 1344 TTTGTAGGCTGGCTCCACATGGAATCTGTGTGTGCGCGCTTGGCCAGAAAGGCTGCA 1403
Db 1331 TTTGTAGGCTGGCTCCACATGGAATCTGTGTGTGCGCGCTTGGCCAGAAAGGCTGCA 1390
QY 1404 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAGATGGGGATT 1463
Db 1391 AGATGTCGAGTCTCTGGGTGGCTCCAGACTGAGTTCCTTAGCTTCCAGATGGGGATT 1449
QY 1464 CCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTCTTCTTCAAAG 1523
Db 1450 CCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTCTTCTTCAAAG 1509
QY 1524 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGTCGCCGATGAGATGTCTGAGAA 1583
Db 1510 CCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGTCGCCGATGAGATGTCTGAGAA 1569
QY 1584 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAGGACGTTGTGCTTCCGATGAGGCA 1643
Db 1570 TGAGACTTACAGTGCCTGAGCCCTGGCAAAAGTGAGGACGTTGTGCTTCCGATGAGGCA 1629
QY 1644 GGAGTTTACAGCCTTCACTTAGGCCAGTTCCGATGAGTGGCGTCTATTTCGCCACAC 1703
Db 1630 GGAGTTTACAGCCTTCACTTAGGCCAGTTCCGATGAGTGGCGTCTATTTCGCCACAC 1689
QY 1704 CCAGCCCAACCTGCCCACGTTCTCTATTGTTTTCGAGACCCCATTTGCTTTCAGGCTGCC 1763
Db 1690 CCAGCCCAACCTGCCCACGTTCTCTATTGTTTTCGAGACCCCATTTGCTTTCAGGCTGCC 1749
QY 1764 CTTCTGGGCTGTGTTACTCGGCCCTTACTCAGATTTTCCTTGGTGGAGCAACAGTCCAG 1823
Db 1750 CTTCTGGGCTGTGTTACTCGGCCCTTACTCAGATTTTCCTTGGTGGAGCAACAGTCCAG 1809
QY 1824 AGAGGCCACAGTGGGAGTGGCCCTCTCTTAAAGATGACTTTTACATATAAATGTTGATC 1883
Db 1810 AGAGGCCACAGTGGGAGTGGCCCTCTCTTAAAGATGACTTTTACATATAAATGTTGATC 1868

QY 1884 TTCAAAAAAAAA 1895
Db 1869 TTCAAAAAAAAA 1880

RESULT 7

US-10-653-595-90
; Sequence 90, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-653-595-90

Query Match 95.6%; Score 1811.2; DB 17; Length 1892;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1860; Conservative 0; Mismatches 8; Indels 4; Gaps 4;

QY 24 GGACGGGGCGGATCTTCTCGGCCATGAGGAGCCGCGCTGGTCTTCTTCCCTCACT 83
Db 13 GGGACCGGACGGATCTTCTCGGCCATGAGGAGCCGCGCTGGTCTTCTTCCCTCACT 72
QY 84 CTTGAAGTGTCTGCTCTTCTCGCTCTGGCACCTCGCAGCCAGGATTCGACTCAGGCC 143
Db 73 CTTGAAGTGTCTGCTCTTCTCGCTCTGGCACCTCGCAGCCAGGATTCGACTCAGGCC 132
QY 144 CACTCCAGCAGCCCTCTCTCTTCCGATACGAACTACGAACTCTTTCGCACTGTGACTCC 203
Db 133 CACTCCAGCAGCCCTCTCTCTTCCGATACGAACTACGAACTCTTTCGCACTGTGACTCC 192
QY 204 AACCTGGAAGGAGAGACTTACCTGCGTCTCGTGCACCCACCGCTCCCGAATCCAC 263
Db 193 AACCTGGAAGGAGAGACTTACCTGCGTCTCGTGCACCCACCGCTCCCGAATCCAC 252
QY 264 ACTCGTCCAGCTGGACCAATATGAAACCAAGCTTAGTCCCGATGCTGTGCTC 323
Db 253 ACTCGTCCAGCTGGACCAATATGAAACCAAGCTTAGTCCCGATGCTGTGCTC 312
QY 324 CAACTCCCTTATGCTCTCTGTTTGTAGTCTTTTCTGCGAGTTCATCTACCTACCGTTGCTC 383
Db 313 CAACTCCCTTATGCTCTCTGTTTGTAGTCTTTTCTGCGAGTTCATCTACCTACCGTTGCTC 372

384 QY CAACCAAGTCTACTATGCGAAGAGTCTCTGTGTTCCAGCCAGTCTCTATTCTCTCACC 443
373 Db CAACCAAGTCTACTATGCGAAGAGTCTCTGTGTTCCAGCCAGTCTCTATTCTCTCACC 432
444 QY TAACTCTCAAGGAGATGAAGCTTCAGCTGAAGTCTCAACCACCAAGATGACCTCCCC 503
433 Db TAACTCTCAAGGAGATGAAGCTTCAGCTGAAGTCTCAACCACCAAGATGACCTCCCC 492
504 QY CATCTCACCCCACTTCACAGTGACAGACCGCCAGACCTTCCAGCCCTGCGCTGAGAGGCT 563
493 Db CATCTCACCCCACTTCACAGTGACAGACCGCCAGACCTTCCAGCCCTGCGCTGAGAGGCT 552
564 QY CAGCAACAACGTTGAAGAGCTCTCAATCTCTCTTGTCTCCCTGGAGGCCAGGAGCAAGC 623
553 Db CAGCAACAACGTTGAAGAGCTCTCAATCTCTCTTGTCTCCCTGGAGGCCAGGAGCAAGC 612
624 QY GCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAAGGAGGAGGCCAGCAACAAGAA 683
613 Db GCAGAGCAACAGCAGGAGCAAGGAGTGGAGCAAGGAGGAGGCCAGCAACAAGAA 672
684 QY GCAGGAGAGGGGCAAGAACAGCAAGAGGAGCAAGAGGAGGAGGAGGAGGAGCA 743
673 Db GCAGGAGAGGGGCAAGAACAGCAAGAGGAGCAAGAGGAGGAGGAGGAGGAGCA 732
744 QY GGAAGAGGACAGGGGACTAAGAGGAGGAGCGGAGGAGTGTCTCTCAGCTGCAGACAGCTC 803
733 Db GGAAGAGGACAGGGGACTAAGAGGAGGAGCGGAGGAGTGTCTCTCAGCTGCAGACAGCTC 792
804 QY AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGT 863
793 Db AGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTAACCCTTCTCTTTTGTCTCCCGGT 852
864 QY ACAGAGAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGGAGCTCATTCGATCAGC 923
853 Db ACAGAGAGTAGAGTCTACTCTCTATGATATGAGAACATCCAGGAGCTCATTCGATCAGC 912
924 QY CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTACTCGAGAAACCAAAA 983
913 Db CCAGGAAATAGATGAATGAATGAATATATGATGAGAACTCTACTCGAGAAACCAAAA 972
984 QY CCTGCGAGCTTCTGCTGAGTCCGCCACACAGAGGCTTGTGCTGTGCTGTGCTATTCGAT 1043
973 Db CCTGCGAGCTTCTGCTGAGTCCGCCACACAGAGGCTTGTGCTGTGCTGTGCTATTCGAT 1031
1044 QY CGTGGAGATACCTGATATATACCCCAAGCCAGGAGGCTGGAAGTATGAGAGGAGA 1103
1032 Db CGTGGAGATACCTGATATATACCCCAAGCCAGGAGGCTGGAAGTATGAGAGGAGA 1091
1104 QY GATCCTTGTGTTTGGGAAAGTCTGTCAGACGCTTGGGCGGCGACATGCTACCTG 1163
1092 Db GATCCTTGTGTTTGGGAAAGTCTGTCAGACGCTTGGGCGGCGACATGCTACCTG 1151
1164 QY TGCCTCTGTGACTTCTGCTCTCTTGAAGCTGGAGCAGTGCCACTCAGAGGCCAGGCTGCA 1223
1152 Db TGCCTCTGTGACTTCTGCTCTCTTGAAGCTGGAGCAGTGCCACTCAGAGGCCAGGCTGCA 1211
1224 QY GCGGCAACATGAGGACACCTCCCAAGAAGTCTGCTGAGCCCTTGTGCTGCTCCCA 1283
1212 Db GCGGCAACATGAGGACACCTCCCAAGAAGTCTGCTGAGCCCTTGTGCTGCTCCCA 1270
1284 QY GAGCCTGTCCATCGGCAACAGGTAGGTTCCCGAGATCAGGCGGCTTTTACGGGCTGGA 1343
1271 Db GAGCCTGTCCATCGGCAACAGGTAGGTTCCCGAGATCAGGCGGCTTTTACGGGCTGGA 1330
1344 QY TTTGTACGGTGGGCTCCACATGAGCTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGGA 1403
1331 Db TTTGTACGGTGGGCTCCACATGAGCTTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGGA 1390
1404 QY AGATGTCGAGTCTCTGGTGGCTCCAGACTGAGTCTTCTAGTCTTCCAGGATGGGATTT 1463
1391 Db AGATGTCGAGTCTCTGGTGGCTCCAGACTGAGTCTTCTAGTCTTCCAGGATGGGATTT 1449
1464 QY CCTTACCAGATTTGTGACACAGACTATATCCAGTACCCCAAACTACTGTTCTTCAAGAG 1523

1450 Db CCTTACCAGATTTGTGACACAGACTATATCCAGTACCCCAAACTACTGTTCTTCAAAG 1509
1524 QY CCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGCATGAGATGTCTGCAGAA 1583
1510 Db CCAGCAGTGTCTGATGAGAAACCGCAATCGGAAGGTGTCCCGCATGAGATGTCTGCAGAA 1569
1584 QY TGAGACTTACAGTGTGCGCTGAGCCCTGGCAAAAGTGAAGGACGTTGTGCTTTCGATGGAGCCA 1643
1570 Db TGAGACTTACAGTGTGCGCTGAGCCCTGGCAAAAGTGAAGGACGTTGTGCTTTCGATGGAGCCA 1629
1644 QY GGAGTTTCAAGCACTTGAATCTTAGGCGCAGTTCGGATGAGCTGGCGTCTATTCTGCCACAC 1703
1630 Db GGAGTTTCAAGCACTTGAATCTTAGGCGCAGTTCGGATGAGCTGGCGTCTATTCTGCCACAC 1689
1704 QY CCAGCCCAACCTGCCAGCTTCTATTGTTTGTGAGACCCCATGCTTTCAGGCTGCC 1763
1690 Db CCAGCCCAACCTGCCAGCTTCTATTGTTTGTGAGACCCCATGCTTTCAGGCTGCC 1749
1764 QY CTTCTGGGTCTGTTACTCGGCCCTTACTCACAATTTCTTGGGTTGGAGCAACAGTCCCAG 1823
1750 Db CTTCTGGGTCTGTTACTCGGCCCTTACTCACAATTTCTTGGGTTGGAGCAACAGTCCCAG 1809
1824 QY AGAGGCCACAGCTGGGAGCTGGGCCCTCTCTTAAAGATGACTTTTACATAAAATGTTGATC 1883
1810 Db AGAGGCCACAGCTGGGAGCTGGGCCCTCTCTTAAAGATGACTTTTACATAAAATGTTGATC 1868
1884 QY TTTCAAAAAAAA 1895
1869 Db TTTCAAAAAAAA 1880

RESULT 8
US-10-085-117-54
; Sequence 54, Application US/10085117
; Publication No. US200302334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-54

Query Match 86.1%; Score 1632; DB 17; Length 1632;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 ATGAGGAAGCCAGCCGCTGCTTCTTCCCTCACTCTCTGAAGGTGCTGCTCTGCTCTG 108
Db 1 ATGAGGAAGCCAGCCGCTGCTTCTTCCCTCACTCTCTGAAGGTGCTGCTCTGCTCTG 60
QY 109 GCACCTGCGGAGCCAGGATTCGACTAGGCCCCGCACTCCAGGCGCCCTCTCTCTCT 168
Db 61 GCACCTGCGGAGCCAGGATTCGACTAGGCCCCGCACTCCAGGCGCCCTCTCTCTCT 120
QY 169 ACCGAATACGAACGCTTCTTGGCACTGCTGACTCCAACTGGAAGGAGGAGTCTCTC 228
Db 121 ACCGAATACGAACGCTTCTTGGCACTGCTGACTCCAACTGGAAGGAGGAGTCTCTC 180
QY 229 CGTCTCCGTGCAACCCAGGCTGCGGGAATCCACACTCGTCAGGTGAGCAATATGAA 288
Db 181 CGTCTCCGTGCAACCCAGGCTGCGGGAATCCACACTCGTCAGGTGAGCAATATGAA 240

QY	289	AACCA	CGGCTTAGTGCCCGATGTGCTGTCTGCTCAA	CGTCTCTTATGCTCTCTCGTTT	348
Db	241	AACCA	CGGCTTAGTGCCCGATGTGCTGTCTCAA	CGTCTCTTATGCTCTCTCGTTT	300
QY	349	GAGTCTTTCTG	CCAGTTCTACTOACTACCGTTGCTCCAAC	CGTCTACTATGCCAAGA	408
Db	301	GAGTCTTTCTG	CCAGTTCTACTOACTACCGTTGCTCCAAC	CGTCTACTATGCCAAGA	360
QY	409	GTCTGTGTTC	CCAGCGAGTCTTATCTCTCACTTAACACTCT	CAAGGAGATAGAAGCT	468
Db	361	GTCTGTGTTC	CCAGCGAGTCTTATCTCTCACTTAACACTCT	CAAGGAGATAGAAGCT	420
QY	469	TCAGCTGAAGTCT	CAACCCACGATGACTTCCCATCTCA	CGGAGTCTCAAGTGA	528
Db	421	TCAGCTGAAGTCT	CAACCCACGATGACTTCCCATCTCA	CGGAGTCTCAAGTGA	480
QY	529	GRAAGCCGAG	CTTCAGCCCTGCGCTCAGAGGCTCAGCA	CAAGTGAAGTGAAGTGA	588
Db	481	GRAAGCCGAG	CTTCAGCCCTGCGCTCAGAGGCTCAGCA	CAAGTGAAGTGAAGTGA	540
QY	589	CAATCTCTTGT	CCCTGGAGGCGCAGGAGCAAGCGCC	CAAGTGAAGTGAAGTGA	648
Db	541	CAATCTCTTGT	CCCTGGAGGCGCAGGAGCAAGCGCC	CAAGTGAAGTGAAGTGA	600
QY	649	GTGAGACAC	AGGAGCCGACCAAGAACCAAGAGGAGGAG	CAAGTGAAGTGAAGTGA	708
Db	601	GTGAGACAC	AGGAGCCGACCAAGAACCAAGAGGAGGAG	CAAGTGAAGTGAAGTGA	660
QY	709	GAGCAAGAG	GAGGAAAGGAGGAGGAGGAGGAGGAGGAG	CAAGTGAAGTGAAGTGA	768
Db	661	GAGCAAGAG	GAGGAAAGGAGGAGGAGGAGGAGGAGGAG	CAAGTGAAGTGAAGTGA	720
QY	769	GGACGGAGG	CGTGTCTCAGCTGACAGACAGCTCAGAG	CGGAGTGAAGTGAAGTGA	828
Db	721	GGACGGAGG	CGTGTCTCAGCTGACAGACAGCTCAGAG	CGGAGTGAAGTGAAGTGA	780
QY	829	CTATCTCTTAA	CCCTTCTCTTTTGTCTCCCGGCTACGAG	AGTGAAGTGAAGTGA	888
Db	781	CTATCTCTTAA	CCCTTCTCTTTTGTCTCCCGGCTACGAG	AGTGAAGTGAAGTGA	840
QY	889	ATAATGGAG	AACATCCAGAGCTCATTCGATCAGCC	AGGAGTGAAGTGAAGTGA	948
Db	841	ATAATGGAG	AACATCCAGAGCTCATTCGATCAGCC	AGGAGTGAAGTGAAGTGA	900
QY	949	ATATATGAT	GAGACTCTTCTAGAGAAACCAAAAC	CGTGAAGTGAAGTGA	1008
Db	901	ATATATGAT	GAGACTCTTCTAGAGAAACCAAAAC	CGTGAAGTGAAGTGA	960
QY	1009	CACACAGAG	CGCTTGTGTGTCTATTCGATCGTGAG	AACTGAGTGAAGTGA	1068
Db	961	CACACAGAG	CGCTTGTGTGTCTATTCGATCGTGAG	AACTGAGTGAAGTGA	1020
QY	1069	CCACAGC	CAAGGCTCGGAGTACATGAGGAGGAG	ATCTGTGTTGGGAGTGGTC	1128
Db	1021	CCACAGC	CAAGGCTCGGAGTACATGAGGAGGAG	ATCTGTGTTGGGAGTGGTC	1080
QY	1129	TGTGACAGC	CTTGGGCGGACACATGTCTACCTGTG	CCCTCTGTGACTTCTGCTCTTG	1188
Db	1081	TGTGACAGC	CTTGGGCGGACACATGTCTACCTGTG	CCCTCTGTGACTTCTGCTCTTG	1140
QY	1189	AAGCTGAG	CAAGTGCACCTCAGAGCCAGCTGAG	CGGCAAAATGCGACCTCCAC	1248
Db	1141	AAGCTGAG	CAAGTGCACCTCAGAGCCAGCTGAG	CGGCAAAATGCGACCTCCAC	1200
QY	1249	AAGACTCC	CTTTGTAGCCCTTGTGCTCTCCAGAG	CGCTGCCATCGGCAACAGGTA	1308
Db	1201	AAGACTCC	CTTTGTAGCCCTTGTGCTCTCCAGAG	CGCTGCCATCGGCAACAGGTA	1260
QY	1309	GGGTCCCA	GAGATCAGGCGCTTTTACGGGCTG	GAATTTGTACGGTGGGCTCAGATG	1368
Db	1261	GGGTCCCA	GAGATCAGGCGCTTTTACGGGCTG	GAATTTGTACGGTGGGCTCAGATG	1320
QY	1369	TTCTGGT	GTGCCGCTTTGCCAAGAAAGGCTGT	GAGATGTCGAGTCTCTGGGGGCTC	1428

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RESULT 9
US-10-296-115-693
; Sequence 693, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488.725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552.317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 693
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-693

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Query Match	67.1%;	Score 1271.8;	DB 17;	Length 1671;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1273;	Conservative	0;	Mismatches	2;
			Indels	0;
			Gaps	0;
QY	91	GTGCTGCTCTGCTCTGCGACCTGCGCGAGCCAGGATTCGACTCAGGCCCGCACTCCA	150	
Db				
	397	GTGCTGCTCTGCTCTGCGACCTGCGCGAGCCAGGATTCGACTCAGGCCCGCACTCCA	456	
QY	151	GGCAGCCCTCTCTCTCTACCGAATACGAAACGTTCTTCGCACTGCTGACTCCAACTGG	210	
Db				
	457	GGCAGCCCTCTCTCTCTACCGAATACGAAACGTTCTTCGCACTGCTGACTCCAACTGG	516	
QY	211	AAGCGAGAGACTACTGCGCTCTCCGTGCAACCCACGGCTGCCGGATCCCAACCTGC	270	
Db				
	517	AAGCGAGAGACTACTGCGCTCTCCGTGCAACCCACGGCTGCCGGATCCCAACCTGC	576	
QY	271	CAGCTGGACCAATATGAAACACACGGCTAGTGCCGAGTGTGCTGCTCTCCAACTTC	330	
Db				
	577	CAGCTGGACCAATATGAAACACACGGCTAGTGCCGAGTGTGCTGCTCTCCAACTTC	636	
QY	331	CTTATGCTCTCGTTTGTAGTCTTTTCGCCAGTTCACTCACTACCGTTGCTCCACCCAC	390	
Db				
	637	CTTATGCTCTCGTTTGTAGTCTTTTCGCCAGTTCACTCACTACCGTTGCTCCACCCAC	696	
QY	391	GTCTACTATGCCAAGAGAGTCTCTGTGTTCCAGCCAGTCTTATTTCTCACTAACACT	450	
b	697	GTCTACTATGCCAAGAGAGTCTCTGTGTTCCAGCCAGTCTTATTTCTCACTAACACT	756	

QY 762 TAAGGAGGACGGAGCGTGTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACATC 821
DB 13052 TAAGGAGGACGGAGCGTGTGTCTCAGCTGCAGACAGACTCAGAGCCCAAGTTTCACATC 13111
QY 822 TGAATCTCTATCTTCTAACCCCTTCTCTTTTGTCTCCCGGGTACGAGAAAGTAGAGTCTAC 881
DB 13112 TGAATCTCTATCTTCTAACCCCTTCTCTTTTGTCTCCCGGGTACGAGAAAGTAGAGTCTAC 13171
QY 882 TCCTATGATAATGAGAAACATCCAGAGCTCATTCGATCAGCCCGAGAAATAGATCAAT 941
DB 13172 TCCTATGATAATGAGAAACATCCAGAGCTCATTCGATCAGCCCGAGAAATAGATCAAT 13231
QY 942 GAATGAAATATATGATGAGAACTCTTACTGGAGAAACCAAACTCCGAGCTTCTCTGCA 1001
DB 13232 GAATGAAATATATGATGAGAACTCTTACTGGAGAAACCAAACTCCGAGCTTCTCTGCA 13291
QY 1002 GCT 1004
DB 13292 GTT 13294

RESULT 15

US-09-918-995-14842
; Sequence 14842, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14842
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-14842

Query Match 22.9%; Score 433.8; DB 10; Length 469;
Best Local Similarity 96.1%; Pred. No. 6e-121;
Matches 441; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 907 GAGCTCATTCGATCAGCCCGAGGAAATAGATGAAATGAAATATATGATGAGAACTCC 966
DB 11 GAGTTCCTAGCAGCAGNGGNGGAANTCTGAAATGAAATGAAATATATGATGAGAACTCC 70
QY 967 TACTGGAGAAACCAAACTCCGAGCTTCTGAGCTGCCGACACACAGAGCCCTTGCTG 1026
DB 71 TACTGGAGAAACCAAACTCCGAGCTTCTGAGCTGCCGACACACAGAGCCCTTGCTG 130
QY 1027 GTGCTGTGCTATTCGATCGTGAGAAATACCTCATCAACCCCAAGCCCTGCG 1086
DB 131 GTGCTGTGCTATTCGATCGTGAGAAATACCTCATCAACCCCAAGCCCTGCG 190
QY 1087 AAGTACATGGAGAGAGATCCTTGGTTTCGGGAAAGTCGGTCTGTGACAGCCCTTGGGGG 1146
DB 191 AAGTACATGGAGAGAGATCCTTGGTTTCGGGAAAGTCGGTCTGTGACAGCCCTTGGGGG 250
QY 1147 CGACACATGCTACCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCT 1206
DB 251 CGACACATGCTACCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCTCTGTGCT 310
QY 1207 TCAGAGGCCAGCCTGCAGGGCAACAAATGCGACACCTCCCAAGACTCCCTTTGTGAGC 1266

DB 311 TCAGAGGCCAGCCTGCAGGGCAACAAATGCGACACCTCCCAAGACTCCCTTTGTGAGC 370
QY 1267 CCCTTGTCTTGCCTCCAGAGCCCTGTCCATCGGCAACCCAGGTAGGGTCCCGAGAAATCAGGC 1326
DB 371 CCCTTGTCTTGCCTCCAGAGCCCTGTCCATCGGCAACCCAGGTAGGGTCCCGAGAAATCAGGC 430
QY 1327 CGCTTTTACGGGCTGGATTGTACGGTGGGCTCCACATG 1365
DB 431 CGCTTTTACGGGCTGGATTGTACGGTGGGCTCCACATG 469

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Job time: 1102 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
11379.049 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895

Sequence: 1 gttagaggggctgtgttc.....tggatcttcaaaaaa 1895

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsl:*
9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	766	40.4	1076	4	BM564020 AGENCOURT
2	755	39.8	1026	4	BM553910 AGENCOURT
3	754	39.8	1093	4	BM563837 AGENCOURT
4	753	39.7	1037	4	BM554354 AGENCOURT
5	734	38.7	836	4	BM830966 AGENCOURT
6	702	37.0	823	4	BM828365 AGENCOURT
7	682	36.0	1023	4	BM554310 AGENCOURT
8	678	35.8	1012	4	BM554519 AGENCOURT
9	676	35.7	779	4	BM829361 AGENCOURT
10	671	35.4	736	4	BM830145 AGENCOURT
11	670	35.4	827	4	BM520181 AGENCOURT
12	667	35.2	718	4	BM826973 AGENCOURT
13	666	35.1	769	4	BM520377 AGENCOURT
14	665	35.1	891	4	BM520336 AGENCOURT
15	655	34.6	706	4	BM520382 AGENCOURT
16	655	34.6	849	6	CD244111 AGENCOURT
17	651	34.4	847	4	BM829134 AGENCOURT
18	641	33.8	849	4	BM830306 AGENCOURT
19	640	33.8	737	4	BM829870 AGENCOURT
20	638	33.7	689	4	BM829870 AGENCOURT
21	620	32.7	866	4	BM828510 AGENCOURT
22	618	32.6	1029	4	BM560468 AGENCOURT
23	617	32.6	773	4	BM829870 AGENCOURT
24	614	32.4	753	4	BM829635 AGENCOURT

25	608	32.1	918	6	CD359186
26	608	32.1	1122	4	BM553134
27	603	31.8	886	6	CD243482
28	595	31.4	646	4	BI829508
29	591	31.2	762	4	BI463234
30	591	31.2	1074	4	BM563920 AGENCOURT
31	589	31.1	640	4	BI829306
32	589	31.1	855	4	BI561292
33	583	29.7	991	4	BI825474
34	562	29.7	658	4	BI828527
35	556	29.3	753	4	BI828527
36	554	29.2	675	4	BI520903
37	550	29.0	910	4	BI832341
38	549	29.0	860	4	BI831640
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41	537	28.3	854	4	BI826371
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43	529	27.9	529	1	AI024421
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51	469	24.7	589	5	BP217972
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53	465	24.5	892	6	CD557111
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73	334	17.6	467	1	AI141116
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82	296	15.6	354	1	AA406076
83	285	15.0	361	1	AA433593
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87	227	12.0	471	1	AA993247
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92	189	10.0	460	2	BF376156
93	174	9.2	426	1	AL597087
94	165	8.7	408	2	BF376146
95	162	8.5	162	1	AI382680
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BI829508	603080338
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102	99	4.7	348	7	R07740	175	22	1.2	647	1	AV260707	AV260707	AV260707
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111	41	2.2	577	2	B1986226	184	22	1.2	767	7	CF739036	CF739036	CF739036
112	40	2.2	445	2	BE233231	185	22	1.2	768	5	BX316397	BX316397	BX316397
113	40	2.1	513	1	AL042116	186	22	1.2	788	5	BX318807	BX318807	AGENCOURT
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120	34	1.8	405	6	CB811133	193	22	1.2	1464	2	BF118779	BF118779	BF118779
121	34	1.8	412	7	CR473065	194	22	1.2	3185	3	AK053586	AK053586	Mus muscu
122	34	1.8	462	4	BI541194	c 195	21	1.1	31	1	AA621303	AA621303	zu83906.s
123	33	1.7	115	1	AA992230	c 196	21	1.1	40	1	A1208979	A1208979	zu83906.s
124	31	1.6	349	4	BM541067	197	21	1.1	211	9	CL478010	CL478010	SAIL 284
125	31	1.6	417	1	A1573445	198	21	1.1	341	1	AA645568	AA645568	aa24e06.f
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127	31	1.6	533	7	CO607922	c 200	21	1.1	407	2	AM630546	AM630546	hb84d06.y
128	31	1.6	575	7	CO597003	c 201	21	1.1	452	9	BF773770	BF773770	28272 MA
129	31	1.6	584	7	CO595610	c 202	21	1.1	452	9	CL873583	CL873583	ade89h02.
130	31	1.6	615	7	CO595171	c 203	21	1.1	475	8	AZ170397	AZ170397	SP 0116.A
131	31	1.6	623	7	CO601955	c 204	21	1.1	475	8	AA640562	AA640562	nt-99d10.s
132	31	1.6	719	9	CE286339	c 205	21	1.1	497	2	BF443476	BF443476	260972 MA
133	29	1.5	582	4	BM537627	c 206	21	1.1	513	2	BE223089	BE223089	hu47b05.x
134	26	1.4	306	7	CO604503	c 207	21	1.1	550	4	BI679826	BI679826	457073 MA
135	26	1.4	758	7	CK469251	c 208	21	1.1	563	1	AI300103	AI300103	qm59g11.x
136	26	1.4	770	7	CK598900	c 209	21	1.1	563	1	AI743822	AI743822	w342c07.x
137	26	1.4	792	8	BZ226260	c 210	21	1.1	568	5	BM968328	BM968328	UI-CF-DUI
138	26	1.4	797	7	CK604050	c 211	21	1.1	582	8	AZ337449	AZ337449	1M0068E12
139	26	1.4	836	7	CK598106	c 212	21	1.1	601	1	AL674723	AL674723	AL674723
140	26	1.4	857	7	CK471040	c 213	21	1.1	607	1	AL896981	AL896981	AL896981
141	24	1.3	358	8	AZ846675	c 214	21	1.1	610	4	BG491920	BG491920	602535835
142	24	1.3	369	5	BY061518	c 215	21	1.1	636	7	CM075310	CM075310	601298733
143	24	1.3	647	8	AZ359345	c 216	21	1.1	639	5	BQ015325	BQ015325	UI-H-ED1-
144	23	1.2	564	2	BE111104	c 217	21	1.1	647	5	BX267049	BX267049	BX267049
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146	23	1.2	667	7	CK843994	c 219	21	1.1	667	5	BX267049	BX267049	BX267049
147	23	1.2	695	1	AV092095	c 220	21	1.1	667	5	BX267049	BX267049	BX267049
148	23	1.2	745	5	BM950309	c 221	21	1.1	667	5	BX267049	BX267049	BX267049
149	23	1.2	792	7	CK595043	c 222	21	1.1	667	5	BX267049	BX267049	BX267049
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151	22	1.2	179	2	AW188855	c 224	21	1.1	667	5	BX267049	BX267049	BX267049
152	22	1.2	239	2	BF152647	c 225	21	1.1	667	5	BX267049	BX267049	BX267049
153	22	1.2	251	7	CK866683	c 226	21	1.1	667	5	BX267049	BX267049	BX267049
154	22	1.2	282	2	BB574057	c 227	21	1.1	667	5	BX267049	BX267049	BX267049
155	22	1.2	266	2	BB564350	c 228	21	1.1	667	5	BX267049	BX267049	BX267049
156	22	1.2	306	7	CF104508	c 229	21	1.1	667	5	BX267049	BX267049	BX267049
157	22	1.2	331	2	BE046182	c 230	21	1.1	667	5	BX267049	BX267049	BX267049
158	22	1.2	363	5	BY093354	c 231	21	1.1	667	5	BX267049	BX267049	BX267049
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160	22	1.2	371	5	BP770016	c 233	21	1.1	667	5	BX267049	BX267049	BX267049
161	22	1.2	416	2	BF021888	c 234	21	1.1	667	5	BX267049	BX267049	BX267049
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163	22	1.2	459	4	BM288266	c 236	21	1.1	667	5	BX267049	BX267049	BX267049
164	22	1.2	470	9	CR262336	c 237	21	1.1	667	5	BX267049	BX267049	BX267049
165	22	1.2	511	1	AV005781	c 238	21	1.1	667	5	BX267049	BX267049	BX267049
166	22	1.2	517	1	AI553526	c 239	21	1.1	667	5	BX267049	BX267049	BX267049
167	22	1.2	523	9	CR138551	c 240	21	1.1	667	5	BX267049	BX267049	BX267049
168	22	1.2	544	8	AZ252213	c 241	21	1.1	667	5	BX267049	BX267049	BX267049
169	22	1.2	570	9	CE671990	c 242	21	1.1	667	5	BX267049	BX267049	BX267049
170	22	1.2	579	7	CF157497	c 243	21	1.1	667	5	BX267049	BX267049	BX267049

244	21	1.1	948	5	BX394390	BX394390 BX394390	C 317	20	1.1	413	2	BB740843
245	21	1.1	958	1	AL562857	AL562857 BX394390	C 318	20	1.1	425	6	BY692699
246	21	1.1	979	5	BX458436	BX458436 BX458436	C 319	20	1.1	426	1	AV808145
247	21	1.1	991	5	BQ072169	AGENCOURT	C 320	20	1.1	426	5	BY283318
248	21	1.1	992	4	BM558887	AGENCOURT	C 321	20	1.1	429	1	AA162353
249	21	1.1	1001	2	BF689251	BF689251 602185042	C 322	20	1.1	432	6	BY693848
250	21	1.1	1005	5	BX399152	BX399152 BX399152	C 323	20	1.1	433	1	AV808047
251	21	1.1	1015	5	BX394389	BX394389 BX394389	C 324	20	1.1	434	8	CC016767
252	21	1.1	1018	5	BK375576	BK375576 BX375576	C 325	20	1.1	435	6	BY579732
253	21	1.1	1022	1	AL567135	AL567135 AL567135	C 326	20	1.1	435	5	BY579732
254	21	1.1	1030	1	AL580458	AL580458 AL580458	C 327	20	1.1	438	9	CL952245
255	21	1.1	1060	8	CC272654	CC272654 CH261-121	C 328	20	1.1	441	6	BY548394
256	21	1.1	1070	4	BM557214	BM557214 AGENCOURT	C 329	20	1.1	442	9	AG192277
257	21	1.1	1072	1	AL562840	AL562840 AL562840	C 330	20	1.1	443	5	BP618329
258	21	1.1	1077	5	BX446398	BX446398 BX446398	C 331	20	1.1	445	6	BY532172
259	21	1.1	1108	1	AL539134	AL539134 BX39134	C 332	20	1.1	446	2	BB785776
260	21	1.1	1106	5	BK358634	BK358634 BX358634	C 333	20	1.1	448	2	BB779924
261	21	1.1	1144	4	BM554390	BM554390 AGENCOURT	C 334	20	1.1	449	9	AG198077
262	21	1.1	1153	5	BM911580	BM911580 AGENCOURT	C 335	20	1.1	453	1	AV791304
263	21	1.1	1165	5	BM916435	BM916435 AGENCOURT	C 336	20	1.1	454	7	CR756533
264	21	1.1	1256	3	CR610727	full-leng	C 337	20	1.1	454	7	CR757049
265	21	1.1	1679	3	AF113672	Homo sapi	C 338	20	1.1	454	7	CR757052
266	21	1.1	1734	3	CR594170	full-leng	C 339	20	1.1	454	7	CR757267
267	20	1.1	138	2	BF399123	UI-R-CAL-	C 340	20	1.1	454	7	CR757779
268	20	1.1	187	1	AI125674	qg90G05.X	C 341	20	1.1	454	7	CR757782
269	20	1.1	194	2	BF309565	BF309565 BF309565	C 342	20	1.1	456	2	BF403476
270	20	1.1	208	7	CF159511	B0673809-	C 343	20	1.1	458	6	BY570154
271	20	1.1	233	9	CG410901	TP2D0017	C 344	20	1.1	464	6	C98732
272	20	1.1	235	1	AV381063	AV381063 BV381063	C 345	20	1.1	467	1	AI840282
273	20	1.1	246	2	AW860616	QVO-C7038	C 346	20	1.1	467	2	BE228381
274	20	1.1	256	9	CE635060	tigr-g88-	C 347	20	1.1	470	8	BH841392
275	20	1.1	275	2	BB354005	BB354005	C 348	20	1.1	470	8	BH841392
276	20	1.1	285	2	BB311479	BB311479 BB311479	C 349	20	1.1	470	8	BH842177
277	20	1.1	292	2	BB434848	BB434848 BB434848	C 350	20	1.1	471	1	BH859000
278	20	1.1	294	2	BB302012	BB302012	C 351	20	1.1	476	2	BF399890
279	20	1.1	295	2	BB192935	BB192935 BB192935	C 352	20	1.1	482	1	AA270689
280	20	1.1	295	2	BB262387	BB262387	C 353	20	1.1	483	4	AA270689
281	20	1.1	296	2	BB087518	BB087518 BB087518	C 354	20	1.1	499	1	AV549047
282	20	1.1	298	2	BB310445	BB310445	C 355	20	1.1	501	1	AA672243
283	20	1.1	299	2	BB222595	BB222595 BB222595	C 356	20	1.1	508	8	AZ846524
284	20	1.1	303	1	AV044452	AV044452 AV044452	C 357	20	1.1	510	8	BH025702
285	20	1.1	306	1	AV146700	AV146700 AV146700	C 358	20	1.1	516	2	BE652261
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288	20	1.1	314	2	BB508248	BB508248 BB508248	C 361	20	1.1	521	6	CA395411
289	20	1.1	316	2	BB311384	BB311384 BB311384	C 362	20	1.1	521	8	B95391
290	20	1.1	320	2	BB220475	BB220475 BB220475	C 363	20	1.1	526	8	AY127380
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292	20	1.1	323	2	BB319094	BB319094 BB319094	C 365	20	1.1	539	9	CL355340
293	20	1.1	326	1	AA198159	AA198159 mv46C07.X	C 366	20	1.1	541	6	CD804541
294	20	1.1	326	1	BB315971	BB315971 BB315971	C 367	20	1.1	542	2	BB821344
295	20	1.1	326	5	BP427995	BP427995 BP427995	C 368	20	1.1	544	4	BM502825
296	20	1.1	328	6	CA960692	TGESTzyel	C 369	20	1.1	547	2	BB767095
297	20	1.1	329	1	AI849070	AI849070 UI-M-AH1-	C 370	20	1.1	551	5	BP370198
298	20	1.1	329	2	BB320304	BB320304 BB320304	C 371	20	1.1	551	6	CB259324
299	20	1.1	330	2	BB551533	BB551533 BB551533	C 372	20	1.1	552	1	AJ801501
300	20	1.1	345	5	BX629749	BX629749 BX629749	C 373	20	1.1	556	1	AV562174
301	20	1.1	347	1	AA204081	AA204081 mu26G01.X	C 374	20	1.1	558	4	BI420420
302	20	1.1	350	1	AI006481	AI006481 ua73D09.X	C 375	20	1.1	558	4	BI420550
303	20	1.1	356	1	AA143967	AA143967 mq53F09.X	C 376	20	1.1	572	1	AV533224
304	20	1.1	364	5	BY415972	BY415972 BY415972	C 377	20	1.1	572	5	BQ552867
305	20	1.1	380	5	BY154810	BY154810 BY154810	C 378	20	1.1	574	4	BI593579
306	20	1.1	383	1	AU040498	AU040498 AU040498	C 379	20	1.1	581	9	CE471060
307	20	1.1	387	5	BX440108	BX440108 BX440108	C 380	20	1.1	588	5	BU219309
308	20	1.1	390	2	BF399015	BF399015 UI-R-CAL-	C 381	20	1.1	589	8	BH334793
309	20	1.1	393	6	BY684146	BY684146 BY684146	C 382	20	1.1	590	5	BQ445107
310	20	1.1	394	8	AQ074596	CIT-HSP-2	C 383	20	1.1	591	9	CR139899
311	20	1.1	399	2	BB741438	BB741438 BB741438	C 384	20	1.1	595	1	AI648096
312	20	1.1	400	5	BY523060	BY523060 BY523060	C 385	20	1.1	606	2	AW584044
313	20	1.1	404	5	BY521869	BY521869 BY521869	C 386	20	1.1	611	2	BF466965
314	20	1.1	407	5	BY437543	BY437543 BY437543	C 387	20	1.1	613	8	BH521075
315	20	1.1	408	1	AU041562	AU041562 AU041562	C 388	20	1.1	615	8	AZ618875
316	20	1.1	411	6	BY613336	BY613336 BY613336	C 389	20	1.1	619	5	BU383085

C 390	20	1.1	624	4	BI617619	BI617619 RH48011.5	C 463	19	1.0	286	1	AV009586
C 391	20	1.1	626	5	BU207876	BU207876 604156159	C 464	19	1.0	289	8	BH226730
C 392	20	1.1	628	9	CE207792	CE207792 tigr-gss-	C 465	19	1.0	296	7	TO1789
C 393	20	1.1	630	2	BH226025	BH226025 BH226025	C 466	19	1.0	300	1	AV177811
C 394	20	1.1	630	5	BP132780	BP132780 AV182101	C 467	19	1.0	300	1	AV177811
C 395	20	1.1	633	1	AV783144	AV783144 AV182101	C 468	19	1.0	300	1	AV182101
C 396	20	1.1	636	6	BY724479	BY724479 BY724479	C 469	19	1.0	303	4	BI399942
C 397	20	1.1	645	1	AI790218	AI790218 UK57D03.X	C 470	19	1.0	308	1	BI399942
C 398	20	1.1	652	4	BJ089214	BJ089214 BJ089214	C 471	19	1.0	308	1	BI399942
C 399	20	1.1	652	7	CN524895	CN524895 UI-M-GHO-	C 472	19	1.0	309	9	CL406443
C 400	20	1.1	662	5	BM949032	BM949032 UI-M-GHO-	C 473	19	1.0	311	9	CE220476
C 401	20	1.1	662	5	BM949032	BM949032 UI-M-GHO-	C 474	19	1.0	326	1	AL046395
C 402	20	1.1	670	6	CL321038	CL321038 CH242.15E	C 475	19	1.0	326	4	BI347814
C 403	20	1.1	675	9	CC482231	CC482231 UI-M-GVO-	C 476	19	1.0	329	5	BY191577
C 404	20	1.1	678	6	CD774482	CD774482 CH240.310	C 477	19	1.0	332	7	BH312074
C 405	20	1.1	681	1	AI788958	AI788958 UK56B09.X	C 478	19	1.0	332	7	CA466874
C 406	20	1.1	684	1	AI547206	AI547206 PN3.1.02	C 479	19	1.0	336	2	BH645761
C 407	20	1.1	702	7	CF532249	CF532249 UI-M-GHO-	C 480	19	1.0	337	2	BF193883
C 408	20	1.1	704	5	BU260507	BU260507 603504760	C 481	19	1.0	339	1	AI242332
C 409	20	1.1	704	5	BU260507	BU260507 603504760	C 482	19	1.0	343	8	BZ955950
C 410	20	1.1	707	8	BZ425814	BZ425814 LjPES11d7	C 483	19	1.0	344	9	CL411414
C 411	20	1.1	708	5	BQ552868	BQ552868 HONPR87TF	C 484	19	1.0	349	2	BF857129
C 412	20	1.1	709	6	BY761465	BY761465 HONPR87TF	C 485	19	1.0	351	1	AI565157
C 413	20	1.1	719	5	BU222881	BU222881 603798242	C 486	19	1.0	358	9	TA98A09P
C 414	20	1.1	728	9	CE017102	CE017102 tigr-gss-	C 487	19	1.0	360	1	AV194747
C 415	20	1.1	741	5	BU228653	BU228653 603495045	C 488	19	1.0	360	1	AV201267
C 416	20	1.1	744	5	BU140329	BU140329 603134014	C 489	19	1.0	363	8	BH064023
C 417	20	1.1	753	7	CF744376	CF744376 UI-M-GVO-	C 490	19	1.0	372	2	BE935075
C 418	20	1.1	754	5	BU272772	BU272772 603494529	C 491	19	1.0	372	9	EX973961
C 419	20	1.1	766	8	BZ436444	BZ436444 HONB41TR	C 492	19	1.0	373	2	CR068837
C 420	20	1.1	774	5	BU386518	BU386518 603856722	C 493	19	1.0	373	1	AI659595
C 421	20	1.1	778	7	CO421662	CO421662 GGEZHT102	C 494	19	1.0	373	2	BF222225
C 422	20	1.1	783	9	CS581875	CS581875 tigr-gss-	C 495	19	1.0	378	1	AA201535
C 423	20	1.1	785	6	CS954150	CS954150 AGENCOURT	C 496	19	1.0	380	5	BU810799
C 424	20	1.1	794	8	AQ746766	AQ746766 HS.2276.A	C 497	19	1.0	383	4	BG119017
C 425	20	1.1	796	7	CE204292	CE204292 R8909151	C 498	19	1.0	383	8	BH35804
C 426	20	1.1	803	5	BU383161	BU383161 603583126	C 499	19	1.0	385	4	BI001198
C 427	20	1.1	808	7	CK119755	CK119755 201C15.P1	C 500	19	1.0	387	2	BF359967
C 428	20	1.1	817	8	BZ448909	BZ448909 BONPS12TR	C 501	19	1.0	391	1	AU219437
C 429	20	1.1	832	8	BZ174367	BZ174367 CH230-268	C 502	19	1.0	393	4	BU146916
C 430	20	1.1	843	9	CL658114	CL658114 PRI0130b	C 503	19	1.0	397	1	AA523230
C 431	20	1.1	850	9	CNS04L1L	CL295554 Tetraodon	C 504	19	1.0	400	6	BY603807
C 432	20	1.1	881	5	BU231563	BU231563 603796517	C 505	19	1.0	400	5	BQ598211
C 433	20	1.1	888	1	AU079261	AU079261 AU079261	C 506	19	1.0	401	1	AI047576
C 434	20	1.1	912	7	CF518026	CF518026 CAP0006.1	C 507	19	1.0	402	1	CE181843
C 435	20	1.1	937	6	CD779104	CD779104 EST650465	C 508	19	1.0	403	9	AL024186
C 436	20	1.1	945	9	BG847974	BG847974 1024019H1	C 509	19	1.0	403	4	BG318830
C 437	20	1.1	951	6	CD796981	CD796981 AGENTCOURT	C 510	19	1.0	406	1	AX098302
C 438	20	1.1	960	5	BU515004	BU515004 AGENCOURT	C 511	19	1.0	408	4	BG319141
C 439	20	1.1	965	8	AG163602	AG163602 SP.1019.A	C 512	19	1.0	408	7	CO306669
C 440	20	1.1	993	8	CC210107	CC210107 CH261-101	C 513	19	1.0	409	1	AI596940
C 441	20	1.1	1028	8	CC241708	CC241708 CH261-102	C 514	19	1.0	411	1	AI034081
C 442	20	1.1	1091	9	CL049907	CL049907 CH216-71F	C 515	19	1.0	412	6	CB801904
C 443	20	1.1	1100	4	BG112285	BG112285 60282431	C 516	19	1.0	414	7	CF789364
C 444	20	1.1	1261	8	AG163602	AG163602 Pan trogl	C 517	19	1.0	415	9	CE065111
C 445	20	1.1	1292	9	AG163602	AG163602 Arabidops	C 518	19	1.0	418	1	AI596940
C 446	20	1.1	1363	3	CNS09ZCT	AX007700 Mus muscu	C 519	19	1.0	420	4	BI190885
C 447	20	1.1	1472	3	AK007700	AK007700 Mus muscu	C 520	19	1.0	425	8	BI54530
C 448	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 521	19	1.0	427	1	AA469116
C 449	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 522	19	1.0	428	4	BG234709
C 450	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 523	19	1.0	429	5	BE200434
C 451	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 524	19	1.0	429	2	BE200434
C 452	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 525	19	1.0	430	2	BF83014
C 453	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 526	19	1.0	432	2	BE950133
C 454	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 527	19	1.0	432	7	BE950133
C 455	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 528	19	1.0	432	2	BE950133
C 456	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 529	19	1.0	432	7	BE950133
C 457	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 530	19	1.0	432	7	BE950133
C 458	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 531	19	1.0	432	7	BE950133
C 459	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 532	19	1.0	432	7	BE950133
C 460	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 533	19	1.0	432	7	BE950133
C 461	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 534	19	1.0	432	7	BE950133
C 462	20	1.1	1530	3	AK048151	AK048151 Mus muscu	C 535	19	1.0	432	7	BE950133

C 536	19	1.0	436	1	AA089129	AA089129	mx57h08.r	609	19	1.0	551	4	BG317960	BG317960	NXPV_007
C 537	19	1.0	439	4	BG039896	BG039896	NXSI_105	C 610	19	1.0	555	5	AA530375	AA530375	VJ48C05.i
C 538	19	1.0	444	7	CO131078	CO131078	EX050644.i	C 611	19	1.0	556	5	BX515394	BX515394	SD07205.3
C 539	19	1.0	446	1	AA221606	AA221606	mw50A02.i	612	19	1.0	557	4	BG639831	BG639831	SD07205.3
540	19	1.0	446	2	BE997181	BE997181	NXCI_107	613	19	1.0	558	1	AI455519	AI455519	LD24677.3
541	19	1.0	447	1	AI315118	AI315118	u129B08.x	614	19	1.0	559	8	QA071138	QA071138	CTIBI-E1
C 542	19	1.0	449	1	AA559011	AA559011	ae41e10.s	615	19	1.0	560	8	AQ700627	AQ700627	HS_5379.A
543	19	1.0	449	5	BQ696718	BQ696718	NXPV_045	C 616	19	1.0	561	9	CR109242	CR109242	Forward_s
544	19	1.0	450	1	AI174037	AI174037	u67501.x	617	19	1.0	562	4	BG546447	BG546447	602573790
545	19	1.0	452	4	BW764395	BW764395	K-ES00045	C 618	19	1.0	562	8	AZ983482	AZ983482	2M0264108
546	19	1.0	454	1	AI681144	AI681144	tx44d11.x	C 619	19	1.0	564	4	BI331414	BI331414	602981711
547	19	1.0	454	7	CO303130	CO303130	EX240122.i	C 620	19	1.0	564	8	BH274165	BH274165	CH230-35C
C 548	19	1.0	456	1	AA250480	AA250480	mw59f03.r	C 621	19	1.0	569	5	BQ490376	BQ490376	92-E9437-
549	19	1.0	456	7	CO331763	CO331763	EX01638.s	C 622	19	1.0	570	4	BI122426	BI122426	1006P61P
C 550	19	1.0	458	6	BX530685	BX530685	BV530685	623	19	1.0	571	5	BU696780	BU696780	LI2in1313
C 551	19	1.0	459	5	EX255067	EX255067	BX255067	624	19	1.0	575	1	AI511712	AI511712	LI43204.5
552	19	1.0	461	2	BF510029	BF510029	UI-H-B14	C 625	19	1.0	579	7	CR904083	CR904083	1e72e06.x
553	19	1.0	461	4	BI805021	BI805021	SO03G10.S	626	19	1.0	580	7	CF793841	CF793841	889290.MA
C 554	19	1.0	469	6	CB679745	CB679745	QJNBF03K	627	19	1.0	582	5	BP206022	BP206022	BP206022
555	19	1.0	472	6	CA657032	CA657032	w1m0.pk00	628	19	1.0	582	5	BP133328	BP133328	BP133328
556	19	1.0	475	7	CN311053	CN311053	170006002	C 629	19	1.0	582	9	CG986652	CG986652	CH240_157
557	19	1.0	477	1	AJ654960	AJ654960	AJ654960	630	19	1.0	582	9	CL337635	CL337635	RFC144_26
558	19	1.0	481	8	AQ524247	AQ524247	HS_5234.B	631	19	1.0	585	1	AI315057	AI315057	u128h06.x
559	19	1.0	483	4	BI359750	BI359750	384416.MA	C 632	19	1.0	589	1	AU213220	AU213220	AU213220
560	19	1.0	486	1	AA816758	AA816758	LD08464.5	633	19	1.0	589	4	BI165134	BI165134	RX04956.5
C 561	19	1.0	486	7	CF792480	CF792480	885418.MA	634	19	1.0	592	9	BI154152	BI154152	Danio.rer
C 562	19	1.0	489	1	AI804518	AI804518	tp60c07.x	635	19	1.0	594	2	BE444330	BE444330	WHE1117.H
C 563	19	1.0	490	9	CE129411	CE129411	tigr-g88-	636	19	1.0	595	4	BI374587	BI374587	R82221.5
564	19	1.0	491	1	AI480764	AI480764	VJ29A09.x	637	19	1.0	597	8	CC417598	CC417598	PUOAG8TD
565	19	1.0	491	1	AA439254	AA439254	LD13766.5	638	19	1.0	599	1	AV668373	AV668373	AV668373
C 566	19	1.0	491	9	CL198609	CL198609	ZMWBBC007	639	19	1.0	600	6	CA776531	CA776531	ip06d01.y
567	19	1.0	492	8	AZ246758	AZ246758	RPCI-23-7	640	19	1.0	601	1	AA392719	AA392719	LD11833.5
C 568	19	1.0	492	9	CC961058	CC961058	BOICL58TR	641	19	1.0	601	9	CE374645	CE374645	tigr-g88-
C 569	19	1.0	493	4	BI403284	BI403284	MI-P-CPI-	642	19	1.0	603	1	AA950740	AA950740	LD30848.5
570	19	1.0	494	4	BI364519	BI364519	RS49660.5	643	19	1.0	603	9	AA392383	AA392383	LD11236.5
C 571	19	1.0	494	7	CO239216	CO239216	WS00725.B	644	19	1.0	603	9	CE378818	CE378818	tigr-g88-
C 572	19	1.0	496	8	AZ921202	AZ921202	1006024G1	645	19	1.0	604	7	CO473667	CO473667	G000410.B
C 573	19	1.0	498	2	BE138353	BE138353	u51f08.y	646	19	1.0	606	6	CA037844	CA037844	HFG829.H
C 574	19	1.0	500	9	CR503318	CR503318	Medicago	647	19	1.0	610	8	AZ382187	AZ382187	IM0139D07
575	19	1.0	502	4	BI643835	BI643835	NXPV_123	648	19	1.0	611	7	CR369651	CR369651	CR369651
C 576	19	1.0	504	7	CF430686	CF430686	NIT1_3_DO	649	19	1.0	611	8	B94389	B94389	CIT-HSP-217
577	19	1.0	506	2	BF733307	BF733307	MR1-AN003	650	19	1.0	617	7	CK528231	CK528231	rsfwf0.00
578	19	1.0	506	8	AQ373107	AQ373107	RPCI11-14	651	19	1.0	617	7	CK998658	CK998658	ip34c11.b
579	19	1.0	507	7	CN335823	CN335823	170005999	652	19	1.0	619	4	BJ498602	BJ498602	BX498602
580	19	1.0	508	1	AI315315	AI315315	u137b02.x	C 653	19	1.0	620	5	BX984555	BX984555	BX984555
581	19	1.0	509	4	BG039820	BG039820	NXSI_101	C 654	19	1.0	620	8	AZ166858	AZ166858	SP_0094.A
C 582	19	1.0	512	8	AZ001768	AZ001768	RPCI-23-3	655	19	1.0	620	8	CE502502	CE502502	tigr-g88-
583	19	1.0	518	6	CD214726	CD214726	pgm2n.pk0	656	19	1.0	621	4	BJ104712	BJ104712	BJ104712
584	19	1.0	519	4	BI483810	BI483810	RE66759.5	657	19	1.0	623	7	CK529240	CK529240	rsfwf0.00
585	19	1.0	519	9	CC623040	CC623040	OGWHM65TV	C 658	19	1.0	624	7	CV031738	CV031738	RTNACLI_3
586	19	1.0	523	4	BG149637	BG149637	nsd31f03.	C 659	19	1.0	624	7	BZ944337	BZ944337	CH240_83C
587	19	1.0	524	4	BI173716	BI173716	RE16805.5	660	19	1.0	624	8	AZ210619	AZ210619	SP_0154.A
588	19	1.0	524	4	BI374007	BI374007	RE61506.5	661	19	1.0	625	8	CF175766	CF175766	795758.MA
C 589	19	1.0	525	1	AI877402	AI877402	v74c06.r	C 662	19	1.0	626	7	CC483275	CC483275	CH240_312
590	19	1.0	526	7	CK528807	CK528807	rsfwf0.00	C 663	19	1.0	626	9	CE483275	CE483275	CH240_312
591	19	1.0	529	8	AQ664355	AQ664355	HS_5493.B	664	19	1.0	627	1	AJ735373	AJ735373	AJ735373
C 592	19	1.0	529	9	CE152472	CE152472	Medicago	C 665	19	1.0	627	9	CG453622	CG453622	OGTCA76TV
C 593	19	1.0	529	9	CE145466	CE145466	tigr-g88-	666	19	1.0	634	4	BG524191	BG524191	39-89.Ste
C 594	19	1.0	530	8	AQ522658	AQ522658	HS_5208.B	667	19	1.0	636	5	BG695976	BG695976	LI2in1122
595	19	1.0	531	1	AL826570	AL826570	AL826570	C 668	19	1.0	636	9	AG045902	AG045902	Pan.trog1
596	19	1.0	532	8	AZ716224	AZ716224	RPCI-24-1	669	19	1.0	636	9	CG067448	CG067448	PUICO68TD
597	19	1.0	534	4	BI116652	BI116652	602868329	670	19	1.0	637	1	AI518028	AI518028	LI37429.5
598	19	1.0	535	2	BF273102	BF273102	GA_EB001	671	19	1.0	637	8	AZ166781	AZ166781	SP_0094.A
599	19	1.0	537	4	BI126439	BI126439	I075P43P	C 672	19	1.0	637	9	CE172594	CE172594	tigr-g88-
C 600	19	1.0	538	1	AL922732	AL922732	AL922732	673	19	1.0	638	2	BB607654	BB607654	BB607654
601	19	1.0	543	7	CF480542	CF480542	POL1_66.H	674	19	1.0	640	1	AI511849	AI511849	LD43388.5
602	19	1.0	544	7	CE321847	CE321847	tigr-g88-	C 675	19	1.0	640	4	BM153404	BM153404	TCBAP2D11
C 603	19	1.0	545	7	CN233217	CN233217	RJA103H09	C 676	19	1.0	640	5	BQ780302	BQ780302	UI-R-FFO-
C 604	19	1.0	546	4	BI348699	BI348699	ic67907.x	677	19	1.0	642	8	AZ210120	AZ210120	SP_0155.A
605	19	1.0	547	1	AI515163	AI515163	LD46871.5	678	19	1.0	642	9	BX991288	BX991288	Forward.s
606	19	1.0	547	1	AV833182	AV833182	AV833182	679	19	1.0	643	4	BI214360	BI214360	RE20138.5
607	19	1.0	548	7	CF489891	CF489891	POL1_61.F	680	19	1.0	646	8	AZ203691	AZ203691	SP_0084.A
C 608	19	1.0	550	9	CE626093	CE626093	tigr-g88-	C 681	19	1.0	647	1	AV344893	AV344893	AV344893

C 828	19	1.0	819	9	CR813084	CR813084	GR0AAA37C	901	19	1.0	986	4	BG500928	BG500928	602546508
C 829	19	1.0	820	7	CK095581	CK095581	UA15CPA09	902	19	1.0	989	9	CL502732	CL502732	SAIL_715
C 830	19	1.0	823	5	BUI14354	BUI14354	603228692	903	19	1.0	990	9	CNS02DIX	CNS02DIX	AL191886 Tetraodon
C 831	19	1.0	832	7	CV121429	CV121429	AGENCOURT	904	19	1.0	992	8	AZ211627	AZ211627	SP_0156_B
C 832	19	1.0	835	4	BM360519	BM360519	GA_Ea003	905	19	1.0	992	9	CNS01SDN	CNS01SDN	AL105317 Drosophila
C 833	19	1.0	835	8	AZ196528	AZ196528	SP_1032_A	906	19	1.0	1000	8	AZ206650	AZ206650	SP_0105_B
C 834	19	1.0	840	7	CK202020	CK202020	FGAS01054	907	19	1.0	1013	8	AZ139615	AZ139615	SP_0158_A
C 835	19	1.0	842	7	CK201670	CK201670	FGAS01019	908	19	1.0	1018	7	CK029803	CK029803	AGENCOURT
C 836	19	1.0	844	8	BZ165583	BZ165583	CH230-463	909	19	1.0	1020	8	CC276896	CC276896	CH261-134
C 837	19	1.0	845	6	CB181606	CB181606	AGENCOURT	910	19	1.0	1024	8	AZ211616	AZ211616	SP_0156_B
C 838	19	1.0	847	2	CG264863	CG264863	OGWK181TH	911	19	1.0	1025	5	BX3161585	BX3161585	BM922148 AGENCOURT
C 839	19	1.0	847	2	BF784653	BF784653	602110376	912	19	1.0	1030	5	AZ211615	AZ211615	SP_0156_B
C 840	19	1.0	848	8	BZ678071	BZ678071	PUBHD01TD	913	19	1.0	1055	5	BM922148	BM922148	AGENCOURT
C 841	19	1.0	849	9	CR213469	CR213469	Reverse_s	914	19	1.0	1059	8	AZ211624	AZ211624	SP_0156_B
C 842	19	1.0	853	7	KI1732436	KI1732436	603355184	915	19	1.0	1061	7	CK212240	CK212240	FGAS02410
C 843	19	1.0	857	7	CK110608	CK110608	N068G12_P	916	19	1.0	1091	5	BQ071745	BQ071745	AGENCOURT
C 844	19	1.0	858	8	AZ205016	AZ205016	SP_0099_A	917	19	1.0	1124	5	BX338081	BX338081	EX338081
C 845	19	1.0	860	7	CO121415	CO121415	GR_EB02J	918	19	1.0	1135	9	CL648771	CL648771	CH213-194
C 846	19	1.0	862	8	AZ136892	AZ136892	SP_0173_A	919	19	1.0	1335	7	CF935571	CF935571	T-EST-B04
C 847	19	1.0	863	4	BG430953	BG430953	602500253	920	19	1.0	1361	5	BUI194095	BUI194095	AGENCOURT
C 848	19	1.0	867	9	CG315997	CG315997	OGXB864TH	921	19	1.0	1520	3	AK017045	AK017045	Mus muscu
C 849	19	1.0	871	8	AZ207726	AZ207726	SP_0134_A	922	19	1.0	1597	3	CR622066	CR622066	full-leng
C 850	19	1.0	872	5	BX410176	BX410176	EX410176	923	19	1.0	1632	3	CNSLTI1A2	CNSLTI1A2	Homo sapi
C 851	19	1.0	874	9	CR051415	CR051415	Reverse_s	924	19	1.0	1840	3	HSM801841	HSM801841	AL136873 Homo sapi
C 852	19	1.0	876	8	AZ208300	AZ208300	SP_0137_B	925	19	1.0	1927	3	AK002562	AK002562	Mus muscu
C 853	19	1.0	877	4	BG843504	BG843504	102400310	926	19	1.0	2090	3	CR606273	CR606273	full-leng
C 854	19	1.0	877	4	B1218440	B1218440	602937932	927	19	1.0	2212	3	AK053949	AK053949	Mus muscu
C 855	19	1.0	877	8	AZ211622	AZ211622	SP_0156_B	928	19	1.0	2577	9	AY406623	AY406623	Homo sapi
C 856	19	1.0	877	8	BH157783	BH157783	ENTRUS58TR	929	19	1.0	2987	3	AK078263	AK078263	Mus muscu
C 857	19	1.0	883	8	AZ206420	AZ206420	SP_0108_A	930	19	1.0	3201	3	AK081518	AK081518	Mus muscu
C 858	19	1.0	883	8	CC366266	CC366266	PUHFF68TB	931	19	1.0	3223	3	AK082465	AK082465	Mus muscu
C 859	19	1.0	885	6	CA488016	CA488016	AGENCOURT	932	19	1.0	3426	3	BC008491	BC008491	Homo sapi
C 860	19	1.0	886	5	BX371383	BX371383	EX371383	933	19	1.0	3633	3	AK048316	AK048316	Mus muscu
C 861	19	1.0	889	5	BX390137	BX390137	EX390137	934	19	1.0	4203	9	CL978230	CL978230	OSIFCC031
C 862	19	1.0	889	8	AZ139664	AZ139664	SP_0158_A	935	19	1.0	4358	3	BC035041	BC035041	Homo sapi
C 863	19	1.0	890	9	CG144596	CG144596	PUFW235TB	936	19	1.0	4593	3	HSM803561	HSM803561	Homo sapi
C 864	19	1.0	902	4	BG281142	BG281142	602401642	937	19	1.0	4617	3	CR627363	CR627363	Homo sapi
C 865	19	1.0	902	8	AZ135785	AZ135785	SP_0157_B	938	18	0.9	99	1	AI611497	AI611497	tt65a12.x
C 866	19	1.0	907	8	AZ139588	AZ139588	SP_0158_A	939	18	0.9	105	2	AMS90937	AMS90937	hg51c11.x
C 867	19	1.0	913	4	B1247099	B1247099	602960664	940	18	0.9	107	2	BF706776	BF706776	281410_MA
C 868	19	1.0	917	4	BG322219	BG322219	602433550	941	18	0.9	118	8	AQ353514	AQ353514	CITBI-E1
C 869	19	1.0	917	9	CC722737	CC722737	OGLAN23TV	942	18	0.9	119	2	BF365688	BF365688	QV2-NT004
C 870	19	1.0	920	8	AZ139508	AZ139508	SP_0179_B	943	18	0.9	119	6	CA778916	CA778916	MPL384_11
C 871	19	1.0	920	8	AZ139566	AZ139566	SP_0158_A	944	18	0.9	120	1	AI611563	AI611563	tt66b08.x
C 872	19	1.0	921	8	AZ202390	AZ202390	SP_0057_B	945	18	0.9	126	1	AI611367	AI611367	tt67a11.x
C 873	19	1.0	923	8	AZ136660	AZ136660	SP_0158_B	946	18	0.9	126	1	AI611522	AI611522	tt67e03.x
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C 875	19	1.0	926	8	AZ215475	AZ215475	Forward_s	948	18	0.9	129	6	CB298794	CB298794	220026_re
C 876	19	1.0	927	8	BZ973612	BZ973612	PUDFA07TD	949	18	0.9	133	8	AZ263533	AZ263533	RPCI-23-1
C 877	19	1.0	930	6	CA474074	CA474074	AGENCOURT	950	18	0.9	135	1	AL791141	AL791141	AL791141
C 878	19	1.0	933	5	BQ928027	BQ928027	AGENCOURT	951	18	0.9	154	9	CE763376	CE763376	tigr-g88-
C 879	19	1.0	934	4	B1871939	B1871939	603396706	952	18	0.9	155	9	CL893820	CL893820	abg23C05
C 880	19	1.0	936	6	CD251316	CD251316	AGENCOURT	953	18	0.9	162	9	CE805914	CE805914	tigr-g88-
C 881	19	1.0	936	8	AZ157778	AZ157778	SP_0058_A	954	18	0.9	166	2	AW811716	AW811716	IL2-S7016
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C 883	19	1.0	937	4	BG295657	BG295657	602393063	956	18	0.9	177	1	AV227322	AV227322	AV227322
C 884	19	1.0	937	5	BQ212433	BQ212433	AGENCOURT	957	18	0.9	180	9	CC692899	CC692899	OGLCK14TH
C 885	19	1.0	940	8	AZ203165	AZ203165	SP_0080_B	958	18	0.9	186	5	BQ343936	BQ343936	RC4-NT005
C 886	19	1.0	941	4	B1145320	B1145320	602910458	959	18	0.9	195	2	BF817259	BF817259	PM2-CI015
C 887	19	1.0	943	6	CD515661	CD515661	AGENCOURT	960	18	0.9	197	7	CO252720	CO252720	WS00817_B
C 888	19	1.0	943	9	AG511905	AG511905	Mus muscu	961	18	0.9	201	1	AA742524	AA742524	nx29910_B
C 889	19	1.0	948	5	BQ944403	BQ944403	AGENCOURT	962	18	0.9	211	5	BP685773	BP685773	BP685773
C 890	19	1.0	948	8	AZ136379	AZ136379	SP_0170_B	963	18	0.9	212	2	AW875211	AW875211	RCS-PT000
C 891	19	1.0	951	2	BF238329	BF238329	601811692	964	18	0.9	213	5	BP950811	BP950811	BP950811
C 892	19	1.0	952	4	B1739768	B1739768	60362258	965	18	0.9	216	1	AA764963	AA764963	nx277509_s
C 893	19	1.0	961	6	CB997671	CB997671	AGENCOURT	966	18	0.9	216	9	BX947052	BX947052	Arabidops
C 894	19	1.0	963	5	BQ888531	BQ888531	AGENCOURT	967	18	0.9	220	2	BF934424	BF934424	IL5-NT027
C 895	19	1.0	965	8	AZ137595	AZ137595	SP_0174_B	968	18	0.9	220	4	BI050579	BI050579	PM1-NG040
C 896	19	1.0	965	9	CG225386	CG225386	OG2AK64TV	969	18	0.9	223	7	CV198143	CV198143	CGF100396
C 897	19	1.0	967	2	BF301164	BF301164	602029189	970	18	0.9	228	1	AA495039	AA495039	fa05e12_s
C 898	19	1.0	967	9	CG316009	CG316009	OGXB864TV	971	18	0.9	239	7	D79530	D79530	HUM274G10B
C 899	19	1.0	970	8	AZ206232	AZ206232	SP_0105_B	972	18	0.9	241	2	BF771176	BF771176	RC2-IT004
C 900	19	1.0	973	2	BE740861	BE740861	601593087	973	18	0.9	243	5	BP010047	BP010047	BP010047

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974      18      0.9      247      1      AV324605
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980      18      0.9      253      7      CR557267
981      18      0.9      254      7      CE643735
982      18      0.9      255      2      AW872590
983      18      0.9      256      7      CK767555
c 984      18      0.9      257      1      AA632496
985      18      0.9      258      7      CO229696
c 986      18      0.9      259      1      AA888677
987      18      0.9      260      2      BB672130
c 988      18      0.9      261      6      CB485950
989      18      0.9      262      6      CB490595
c 990      18      0.9      263      1      AL642961
c 991      18      0.9      264      5      BP951301
c 992      18      0.9      265      2      BF375343
993      18      0.9      266      7      CO320178
c 994      18      0.9      267      1      AA676301
995      18      0.9      268      2      BE938535
c 996      18      0.9      269      1      AA668196
997      18      0.9      270      2      BE324310
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ALIGNMENTS

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RESULT 1
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LOCUS      AGENCOURT 6560257 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742040
5', mRNA sequence.
ACCESSION      BM564020
VERSION      BM564020.1 GI:18811457
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1076)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-remail.nih.gov
      Tissue Procurement: Life Technologies, Inc.
      cDNA Library Preparation: Life Technologies, Inc.
      DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      Plate: L1AM12759 row: i column: 17
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          Site 2: EcoRV (destroyed); RNA source normal medulla from
          anonymous male age 27. Library is oligo-dT primed and
          directionally cloned (EcoRV site is destroyed upon
          cloning). Average insert size 1.3 kb, insert size range

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FEATURES

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ORIGIN
Query Match      40.4%; Score 766; DB 4; Length 1076;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 816; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      22      CGGGACCGGGCGGAGATCTTCTCCGCCATGAGGAGCAGCGCTTCTCTTCCCTCA 81
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QY      82      CTCCTGAAAGTCTCTCTCTGCTCTGACCTGCGCAGCTGCGCAGCCAGGATTCAGCTCAGGCC 141
DB      81      CTCCTGAAAGTCTCTCTCTGCTCTGACCTGCGCAGCTGCGCAGCCAGGATTCAGCTCAGGCC 140
QY      142      CCACCTCCAGGAGCGCTCTCTCTCTACCGAATACGAACGCTTCTTTCGCACTGCTGACT 201
DB      141      TCCACTCCAGGAGCGCTCTCTCTCTACCGAATACGAACGCTTCTTTCGCACTGCTGACT 200
QY      202      CCAACCTGGAAGGAGGAGACTACCTGCGCTCTCGTGCAACCCACGCTGCGGGAATCCC 261
DB      201      CCAACCTGGAAGGAGGAGACTACCTGCGCTCTCGTGCAACCCACGCTGCGGGAATCCC 260
QY      262      ACATCTGCTCCAGCTGAGCCCAATATGAAAACCAACGCTTAGTGCCGATGCTGCTGTC 321
DB      261      ACATCTGCTCCAGCTGAGCCCAATATGAAAACCAACGCTTAGTGCCGATGCTGCTGTC 320
QY      322      TCCAACTCTCCCTTATGCTCTCTGTTGAGTCTTTCGCACTGCTGCTGCTGCTGCTG 381
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QY      382      TCCAACTCTCTACTATGCAAGAGAGTCTCTGTTTCCGAGCAGCTCTCTATTTCTCA 441
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QY      502      CCCATCTCACCCCACTTTCACAGTGACAGAACCCAGCAGCTTCCAGCCCTGGCTGAGAG 561
DB      501      CCCATCTCACCCCACTTTCACAGTGACAGAACCCAGCAGCTTCCAGCCCTGGCTGAGAG 560
QY      562      CTGAGCAACAACTGGAAGAGTCTTCAATCTCTCTTCTGAGGAGCCAGGAGCAA 621
DB      561      CTGAGCAACAACTGGAAGAGTCTTCAATCTCTCTTCTGAGGAGCCAGGAGCAA 620
QY      622      GCGCCAGAGCACAAGCAGGAGCAAGAGTGGAGCAGGAGGAGCCAGGAGCCAGCAAGAAC 681
DB      621      GCGCCAGAGCACAAGCAGGAGCAAGAGTGGAGCAGGAGGAGCCAGGAGCCAGCAAGAAC 680
QY      682      AGCAGGAAGAGGGGAGCAAGAAAGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGG 741
DB      681      AGCAGGAAGAGGGGAGCAAGAAAGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGG 740
QY      742      CAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 801
DB      741      CAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 800
QY      802      TCAGAGCCCAAGTTTCACTCTGAAATCTCTATCTTCTA 838
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RESULT 2
BM553910
LOCUS
DEFINITION
AGENCOURT 6546785 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742226
5', mRNA sequence.
ACCESSION
BM553910

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VERSION BM553910.1 GI:18793058
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1026)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: a column: 11
High quality sequence stop: 713.
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/clone_lib="NIH MGC 119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 39.8%; Score 755; DB 4; Length 1026;
Best Local Similarity 99.9%; Pred. 0;
Matches 805; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB |||||
QY 61 GCGCTGGCTTCTTCCCTCCTCTGAGGTGCTCTCTGCTTGGCCTTGGCCTGCGCA 120
DB |||||
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DB |||||
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QY 185 CGCTTCTTCGCACTGCTGACTCAACTCGAAGGAGAGACTCTGCGTCTCCGTGCA 244
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QY 241 ACCCAGGCTGGGATCCACATCTGCTCCAGCTGGACCAATATGAAACACGCTTA 300
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DB |||||
QY 301 GTGCCGATGGTGTCTGCTCCACCTCCCTTATGCTCTGCTTTCAGTCTTCTGCG 360
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QY 361 CAGTTCTACTACTAGCGTTGCTCCACACGCTCTACTATGCCAAGAGAGTCTGTGTTCC 420
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FEATURES
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/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

RESULT 3
BM553910.1
LOCUS BM553910.1
DEFINITION AGENCOURT_6560348 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5741926
5', mRNA sequence.
ACCESSION BM553910.1
VERSION BM553910.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1093)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12759 row: d column: 23
High quality sequence start: 11
High quality sequence stop: 724.
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

QY 421 CAGCCAGTCTCTATCTCTCCTCACTACACTCTCAAGGAGATAGAACTTCAGCTGAAGTC 480
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DB |||||
QY 481 TCACCCACACGATGACCTCTCCCTCACTCTCAAGGAGATAGAACTTCAGCTGAAGTC 540
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DB |||||
QY 605 TTCCAGCCCTGCGCTGAGAGGCTCAGCAACAGCTGGAAGAGCTCTTACCAATCTCTCTG 664
DB |||||
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

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(Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

Query Match 39.8%; Score 754; DB 4; Length 1093;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 804; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

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QY	79	TCACCTCTGAAGGTGCTGCTCCTGCTCTGCGACCTGCGCAGCCCAAGGATTTCGACTCAG	138
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QY	139	GCCCGCCACTCCAGGAGCGCTCTCTCTCCTACCGAATACGAACGCTTCTTGCACTGCTG	198
DB	141	GCCTCCACTCCAGGAGCGCTCTCTCTCTACCGAATACGAACGCTTCTTGCACTGCTG	200
QY	199	ACTCCAACTCGAAGGAGAGACTACCTGCGCTCTCGTCAACCCACGCTGCGCGAAT	258
DB	201	ACTCCAACTCGAAGGAGAGACTACCTGCGCTCTCGTCAACCCACGCTGCGCGAAT	260
QY	259	CCGACACTGTGTCAGCTGGACCAATATGA AAAACAACGCGCTAGTGCGCCGATGTGTGTC	318
DB	261	CCGACACTGTGTCAGCTGGACCAATATGA AAAACAACGCGCTAGTGTGCCGATGTGTGTC	320
QY	319	TGCTCCAACTCCCTTATGCTCTGCTGTGAGTCTTCTGCCAGTTCATCTACTACCGT	378
DB	321	TGCTCCAACTCCCTTATGCTCTGCTGTGAGTCTTCTGCCAGTTCATCTACTACCGT	380
QY	379	TGCTCCAAACCACTACTACTATGCCAAGAGAGTCTCTGTGTTCCACGCGAGTCTCTATTCTC	438
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QY	619	CAAGCGCCAGAGCAACAGGAGGACAGGAGTGGAGCACAGGACGAGGCGCACACAGAA	678
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DB	681	CACACAGGAAGAGGGGCGAAGAACAGGAAGAGCAAGAGGAAACAGGAAGAGGAGGGA	740
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DB	801	GACTCAGAGCCCAAGTTTCACTCTG	825

[illegible]

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1037)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 722.
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 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 Kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (invitrogen). Research Genetics tracking code 013. Note
 this is a NIH MGC library."

Query Match 39.7%; Score 753; DB 4; Length 1037;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	39	TTCTCGGCCATGAGGAAGCCAGCGCTGGCTTCTTCCCTCACTCTGAAGGTCTGCT	98
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QY	99	CTGTGCTCTGSCACTTCCGCGACGCCAGAGATTCGACTCAGGCCCCCACTCCAGGCAGGCC	158
Db	86	CTGTGCTCTGSCACTTCCGCGACGCCAGAGATTCGACTCAGGGCTCCACTCCAGGCAGGCC	145
QY	159	TCTCTCTCTACCGAATACGAAGCGCTTCTTGGCACTGCTGACTCCAACTCGGAAGGCAGA	218
Db	146	TCTCTCTCTACCGAATACGAAGCGCTTCTTGGCACTGCTGACTCCAACTCGGAAGGCAGA	205
QY	219	GACTACTTGCCTGCTCCGTGCAACCCAGCGCTGCCGGAATCCCACTCGTCCAGCTGGA	278
Db	206	GACTACTTGCCTGCTCCGTGCAACCCAGCGCTGCCGGAATCCCACTCGTCCAGCTGGA	265
QY	279	CCAAATATGAAAACCAACCGCTTAGTGCCGATGGTGTGCTGCTCCAACTCCCTTTATGC	338
Db	266	CCAAATATGAAAACCAACCGCTTAGTGCCGATGGTGTGCTGCTCCAACTCCCTTTATGC	325
QY	339	CTCTGTGTTTGAGTCTTTCTGCGAGTTCACTCACTACCGTTGCTCCAAACCAAGTCTACTA	398
Db	326	CTCTGTGTTTGAGTCTTTCTGCGAGTTCACTCACTACCGTTGCTCCAAACCAAGTCTACTA	385
QY	399	TGCCAAGAGAGTCTGTGGTTCCAGCGAGTCTTATTCTCTCACTACACTCTCAAGGA	458
Db	386	TGCCAAGAGAGTCTGTGGTTCCAGCGAGTCTTATTCTCTCACTACACTCTCAAGGA	445
QY	459	GATAGAAGCTTCAGCTGAAGTCTTCACCCACCAAGATGACCTCCCGCACTTCACCCCACTT	518

Db	446	GATAGAGCTTCAGCTGAAGTCTCA	CCCAACACGATGACTCTCACCCCACTT	505
Qy	519	CACAGTGACAGAACGCCAGACCTT	CCAGCCCTGGCCTCAGAGGCTCAGCA	578
Db	506	CACAGTGACAGAACGCCAGACCTT	CCAGCCCTGGCCTCAGAGGCTCAGCA	565
Qy	579	AGAGCTCCTACAATCTCTCTTGT	CCCTGGAGGCCAGGAGCAAGCGCCAG	638
Db	566	AGAGCTCCTACAATCTCTCTTGT	CCCTGGAGGCCAGGAGCAAGCGCCAG	625
Qy	639	GGAGCAGGAGTGGAGCACAGCGCA	GAGGCGGACACAAGACACAGACGAG	698
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Qy	699	GAACACAGAGAGCAAGAGAGGAAC	CAGGAGAGGAGGAAGCAGGAGGAAG	758
Db	686	GAACACAGAGAGCAAGAGAGGAAC	CAGGAGAGGAGGAAGCAGGAGGAAG	745
Qy	759	GACTAAGAGAGGACGGGAGGCTGT	GTCTCAGCTGCAGACAGACTCAGAG	818
Db	746	GACTAAGAGAGGACGGGAGGCTGT	GTCTCAGCTGCAGACAGACTCAGAG	805
Qy	819	CTCTGAATCTCTATCTTCTTAACCC		842
Db	806	CTCTGAATCTCTATCTTCTTAACCC		829

RESULT 5			
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LOCUS			
DEFINITION	BI830966	836 bp	mRNA linear EST 04-OCT-2001
	603080803F1	NIH_MGC_119	Homo sapiens cDNA clone IMAGE:5172457 5', mRNA sequence.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 836)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM11429 row: e column: 02
High quality sequence stop: 836.

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        site 2: EcoRV (destroyed); RNA source normal medulla from
        anonymous male age 27. Library is oligo-dT primed and
        directionally cloned (EcoRV site is destroyed upon
        cloning). Average insert size 1.3 kb, insert size range
        0.9-3 kb. Library is normalized and enriched for
        full-length clones and was constructed by C. Gruber
        (Invitrogen). Research Genetics tracking code 013. Note
        this is a NIH MGC Library."

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ORIGIN

Query Match		38.7%	Score 734;	DB 4;	Length 836;
Best Local Similarity		99.8%	Pred. No. 0;		
Matches 834; Conservative		0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	23	GGGACGGGGCGGATCTTCTCCGGCCATGAGGAAGCCAGCGCTGGCTCTCTTCCCTCCAC	82		
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Qy	83	TCCTGAAGGTGCTCTCTGCTCTGGCACTCGCGGAGCCCAAGATTCAGCTCAGGCCC	142		
Db	61	TCCTGAAGGTGCTCTCTGCTCTGGCACTCGCGGAGCCCAAGATTCAGCTCAGGCCC	120		
Qy	143	CCACTCCAGGACGCCCTCTCTCTTACCGAATACGAACGCTTCTTCGCACTGCTGACTC	202		
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Qy	263	CACCTCGTCAGCTGGACCAATATGAAACACACGGCTTAGTGCCGATGGTGCTGTGCT	322		
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Qy	743	AGGAAGAGGACAGGGGACTTAAGGAGGAGCGGAGGCTGTGTCTCAGCTGCAGACAGACT	802		
Db	721	AGGAAGAGGACAGGGGACTTAAGGAGGAGCGGAGGCTGTGTCTCAGCTGCAGACAGACT	780		
Qy	803	CAGAGCCCAAGTTTCACTCTGAATCTCTATCTTCTTAACCCCTTCTCTTTTGTCTCC	858		
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DEFINITION	BI828365 823 bp mRNA linear EST 04-OCT-2001 603078309F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170058 5', mRNA sequence.
ACCESSION	BI828365
VERSION	BI828365.1 GI:159339915
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORIGIN

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Db 81 CACTCTGAGGTGCTGCTCTCTGCTTGGACCTGCGGAGCCAGGATTCAGTCAGG 140
Qy 140 CCCCCACTCCAGGAGCCCTCTCTCTTACCGAATACGAACGCTTCTTCCGACTGCTGA 199
Db 141 CTTCACTCCAGGAGCCCTCTCTCTTACCGAATACGAACGCTTCTTCCGACTGCTGA 200
Qy 200 CTTCAACTGGAAGGAGGAGACTTACTCTGCGGTCTCGTGAACCCAGCGTGCAGGAATC 259
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Db 321 GCTCAACCTCTCCCTTATGCTCTGCTTGTAGTCTTCTGCGAGTTCACCTACCGTT 380
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Db 681 ACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 740
Qy 740 AGCAGGAGGAGG 752
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5', mRNA sequence.
BM554519
VERSION
KEYWORDS
SOURCE
ORGANISM

BM554519 1012 bp mRNA linear EST 20-FEB-2002
AGENCOURT 654640 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742576
5', mRNA sequence.
BM554519
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1012)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12760 row: p column: 01

High quality sequence stop: 673.

FEATURES

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ORIGIN

Query Match 35.8%; Score 678; DB 4; Length 1012;
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Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 35.4%; Score 671; DB 4; Length 736;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 TGATGAACTCTACTGGAGAAACCAAAACCTGCGAGCTTCTGCGAGTGCCTCCACAC 120
QY 1014 AGAGGCTTGTGCTGTGCTATTCGATCTGGAGAAATACCTGATCATATACCCCCAC 1073
DB 121 AGAGGCTTGTGCTGTGCTATTCGATCTGGAGAAATACCTGATCATATACCCCCAC 180
QY 1074 AGCAAGGCTGGAAGTACATGAGGAGGAGATCTTGTGTTTCGGGAAGTGGTCTGTGA 1133
DB 181 AGCAAGGCTGGAAGTACATGAGGAGGAGATCTTGTGTTTCGGGAAGTGGTCTGTGA 240
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DB 301 GGAGCAGTGCCTCAGAGCCAGCTGCGCGGCAACATGCGACACCTCCCAAGAC 360
QY 1254 TCCTTTGTGAGCCCTTGTGCTTCCCTCCAGAGCCTGCTCATCGGCAACAGGTAGGTC 1313
DB 361 TCCTTTGTGAGCCCTTGTGCTTCCCTCCAGAGCCTGCTCATCGGCAACAGGTAGGTC 420
QY 1314 CCAGAAATCAGGCGCTTTTACGGGCTGGATTGTACGGTGGCTCCACATGACTTCTG 1373
DB 421 CCAGAAATCAGGCGCTTTTACGGGCTGGATTGTACGGTGGCTCCACATGACTTCTG 480
QY 1374 GTGTGCCCGCTTGCACGAAAGGCTGTGAAGATGCCAGTCTCTGGGTGGCTCCAGAC 1433
DB 481 GTGTGCCCGCTTGCACGAAAGGCTGTGAAGATGCCAGTCTCTGGGTGGCTCCAGAC 540
QY 1434 TGAGTTTCTTAGCTTCCAGATGGGATTTCCCTACCAAGATTGTGACACAGACTATAT 1493
DB 541 TGAGTTTCTTAGCTTCCAGATGGGATTTCCCTACCAAGATTGTGACACAGACTATAT 600
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DB 601 CCAGTACCCAAACTACTGTTCCTTCAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCG 660
QY 1554 GAAGTGTCCCGATCAGATGTCTGAGAAATGAGACTTACGTGCGCTGAGCCCTGGCAA 1613
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QY 1614 AA 1615
DB 721 AA 722

RESULT 11
BI520181
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LOCUS BI520181 827 bp mRNA linear EST 29-AUG-2001
DEFINITION G03071429F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163366 5',
mRNA sequence.
ACCESSION BI520181
VERSION BI520181.1 GI:15344973
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11405 row: j column: 07
High quality sequence stop: 826.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5163366"
/tissue_type="medulla"
/lab_host="DH108"
/clone_lib="NIH_MGC_119"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 35.4%; Score 670; DB 4; Length 827;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1033 TGCTATTGATCGTGGAGAAATACCTGCATCATACCCACAGCCCAAGGCTGGAAGTAC 1092
DB 1 TGCTATTGATCGTGGAGAAATACCTGCATCATACCCACAGCCCAAGGCTGGAAGTAC 60
QY 1093 ATGGAGGAGGAGATCCTTGGTTTCGGGAAGTGGTGTGACAGCTTGGCGGCGACAC 1152
DB 61 ATGGAGGAGGAGATCCTTGGTTTCGGGAAGTGGTGTGACAGCTTGGCGGCGACAC 120
QY 1153 ATGTCTACCTGTGCTCTGTGACTTCTGCTCTTGAAGCTGGAGCAGTGCCTCAGAG 1212
DB 121 ATGTCTACCTGTGCTCTGTGACTTCTGCTCTTGAAGCTGGAGCAGTGCCTCAGAG 180
QY 1213 GCAGCTGCAGCGGCAACAATGCGACACCTCCCAAGACTCCCTTTGTGAGCCCTTG 1272
DB 181 GCAGCTGCAGCGGCAACAATGCGACACCTCCCAAGACTCCCTTTGTGAGCCCTTG 240
QY 1273 CTTGCTCCAGAGCTGTCCATCGGCAACAGGTAGGTTCCCAAGACTCCGCTTT 1332
DB 241 CTTGCTCCAGAGCTGTCCATCGGCAACAGGTAGGTTCCCAAGACTCCGCTTT 300
QY 1333 TACGGGCTGGATTGTACCGGTGGGCTCCACATGAGACTTCTGCTGTGCCGGCTTGCACG 1392
DB 301 TACGGGCTGGATTGTACCGGTGGGCTCCACATGAGACTTCTGCTGTGCCGGCTTGCACG 360

QY 1393 AAAGGCTGTGAAGATGTCGAGTCTCTGGTGGCTCCAGACTGAGTCTCTTAGCTTCAG 1452
 Db |||||
 QY 1453 GATGGGATTTCCCTACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGT 1512
 Db |||||
 QY 1513 TCCTTCAAAAGCCAGCAGTGTCTGTGATGAGAAACCCGCAATCCGAAAGTGTCCGATGAGA 1572
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 QY 1573 TGTCTCAGAAATGAGACTTACAGTGGCTGAGCCCTGGCAAAAGTGAGAGTGTGTGCTT 1632
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 Db |||||
 QY 1693 TGTGCCCCA 1702
 Db |||||
 661 TCTGCCACA 670

RESULT 12
 LOCUS BI26973
 DEFINITION 718 bp mRNA linear EST 04-OCT-2001
 603075871F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5167696 5',
 mRNA sequence.
 ACCESSION BI26973
 VERSION BI26973.1 GI:15939523
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11416 row: n column: 17
 High quality sequence stop: 684.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:5167696"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

FEATURES

Source
 1..718
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5167696"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match

35.2%; Score 667; DB 4; Length 718;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1228 CAACAATGGACACCTCCCAAGACTCCCTTTGTGACGCCCTTGTCTTGCCTCCAGAGC 1287
 Db |||||
 1 CAACAATGGACACCTCCCAAGACTCCCTTTGTGACGCCCTTGTCTTGCCTCCAGAGC 60
 QY 1288 CTGTCCATCGGCAACCAAGTAGGTCGCCAGAACTCAGCGCCCTTTACGGCTGGATTG 1347
 Db |||||
 61 CTGTCCATCGGCAACCAAGTAGGTCGCCAGAACTCAGCGCCCTTTACGGCTGGATTG 120
 QY 1348 TAGGTGGGCTCCACATGGACTCTTGTGTGTCGCCGCTTGCACGAAAGGCTGTGAAGAT 1407
 Db |||||
 121 TAGGTGGGCTCCACATGGACTCTTGTGTGTCGCCGCTTGCACGAAAGGCTGTGAAGAT 180
 QY 1408 GTCCAGAGTCTCTGGGTGGCTCCAGACTGAGTCTCTTAGCTTCCAGGATGGGATTTCCCT 1467
 Db |||||
 181 GTCCAGAGTCTCTGGGTGGCTCCAGACTGAGTCTCTTAGCTTCCAGGATGGGATTTCCCT 240
 QY 1468 ACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAGCCAG 1527
 Db |||||
 241 ACCAAGATTTGTGACACAGACTATATCCAGTACCCAACTACTGTTCTTCAAAGCCAG 300
 QY 1528 CAGTGTCTGATGAGAAACCCGCAATCGGAAGTGTCCGCAATGATGTCTGCAGAAATGAG 1587
 Db |||||
 301 CAGTGTCTGATGAGAAACCCGCAATCGGAAGTGTCCGCAATGATGTCTGCAGAAATGAG 360
 QY 1588 ACTTACAGTGGCTGAGCCCTGGCAAAAGTGAGAGCTGTGCTTGCATGGAGCCAGGAG 1647
 Db |||||
 361 ACTTACAGTGGCTGAGCCCTGGCAAAAGTGAGAGCTGTGCTTGCATGGAGCCAGGAG 420
 QY 1648 TTGAGCACTTGAATCTAGGCAATGCGGATGAGTGGGCTCTATTCTGCCACACCCCA 1707
 Db |||||
 421 TTGAGCACTTGAATCTAGGCAATGCGGATGAGTGGGCTCTATTCTGCCACACCCCA 480
 QY 1708 GCCCAACTGCCACAGTCTCTATTGTTTGGAGCCCATTTGCTTTCAGCTGCCCTTTC 1767
 Db |||||
 481 GCCCAACTGCCACAGTCTCTATTGTTTGGAGCCCATTTGCTTTCAGCTGCCCTTTC 540
 QY 1768 TGGTCTGTTACTCGGCCCTTACTCAATTCCTGGGTGGAGCAACAGTCCAGAGAG 1827
 Db |||||
 541 TGGTCTGTTACTCGGCCCTTACTCAATTCCTGGGTGGAGCAACAGTCCAGAGAG 600
 QY 1828 GGCCACGCTGGAGCTGGCCCTTAAAGTACTTTACATAAAATGTTGATCTTCA 1887
 Db |||||
 601 GGCCACGCTGGAGCTGGCCCTTAAAGTACTTTACATAAAATGTTGATCTTCA 660
 QY 1888 AAAAAA 1894
 Db |||||
 661 AAAAAA 667

RESULT 13

LOCUS BI20377
 DEFINITION 603071855F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163852 5',
 mRNA sequence.
 ACCESSION BI20377
 VERSION BI20377.1 GI:15345169
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11405 row: n column: 13
 High quality sequence stop: 740.
 Location/Qualifiers
 1. .769
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 /lab_host="DH10B"
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 /note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 35.1%; Score 666; DB 4; Length 769;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 716; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGAGCGGCTTGTCACGGGACGGCGGCGGATCTTCGCGCCATGAGGAGCCA 60
 DB |||||
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 DB |||||
 QY 61 GCGGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGCACCTGCGCA 120
 DB |||||
 QY 86 GCGGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGCACCTGCGCA 145
 DB |||||
 QY 121 GCCCAGGATTCAGCTCAGGCGCCCTCACTCAGGAGCCCTCTCTCTACCGAATACGAA 180
 DB |||||
 QY 146 GCCCAGGATTCAGCTCAGGCGCCCTCACTCAGGAGCCCTCTCTCTACCGAATACGAA 205
 DB |||||
 QY 181 CGCTTCTTCGCACTGTCTGCTCCAACTCGAAGGACAGACTACCTGCGCTCTCGTGCA 240
 DB |||||
 QY 206 CGCTTCTTCGCACTGTCTGCTCCAACTCGAAGGACAGACTACCTGCGCTCTCGTGCA 265
 DB |||||
 QY 241 ACCCAGGCTGCGGAATCCCACTCTGCTGAGCAATATGAAACACCGCTTA 300
 DB |||||
 QY 266 ACCCAGGCTGCGGAATCCCACTCTGCTGAGCAATATGAAACACCGCTTA 325
 DB |||||
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 DB |||||
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 DB |||||
 QY 361 CAGTTCACTCACTACGTTGCTCCACACGCTCTACTATGCAAGAGAGTCTGCTGCTCC 420
 DB |||||
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 DB |||||
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 DB |||||
 QY 446 CAGCCAGTCTCTATTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 505
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 QY 506 TCACCCACCAAGATGATCTCCCTCACTCTCACTCACTCACTCACTCACTCACTCACTCACT 565
 DB |||||
 QY 541 TTCACGCTGCTGAGAGGCTCAGACACAGTGGAGAGCTCTCAATCTCTCTG 600
 DB |||||
 QY 566 TTCACGCTGCTGAGAGGCTCAGACACAGTGGAGAGCTCTCAATCTCTCTG 625
 DB |||||
 QY 601 TCCCTGGAGGCGCAGGAGCAAGCGCCAGAGCAACAGCAGGAGTGGAGCACAGG 660
 DB |||||
 QY 626 TCCCTGGAGGCGCAGGAGCAAGCGCCAGAGCAACAGCAGGAGTGGAGCACAGG 685
 DB |||||

QY 661 CAGGAGCGGCGACACAGACACAGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 717
 DB |||||
 QY 686 CAGGAGCGGCGACACAGACACAGCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 742
 DB |||||

RESULT 14
 BI520136
 LOCUS
 DEFINITION 891 bp mRNA linear EST 29-AUG-2001
 603071275F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163259 5',
 mRNA sequence.
 BI520136
 ACCESSION
 VERSION
 KEYWORDS
 BI520136.1 GI:15344928
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 891)
 NIH-MGC <http://mgi.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11405 row: e column: 20
 High quality sequence stop: 843.
 Location/Qualifiers
 1. .891
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="IMAGE:5163259"
 /tissue_type="medulla"
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 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 35.1%; Score 665; DB 4; Length 891;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGAGCGGCTTGTCACGGGACGGCGGCGGATCTTCGCGCCATGAGGAGCCA 60
 DB |||||
 QY 5 GTTAGAGCGGCTTGTCACGGGACGGCGGCGGATCTTCGCGCCATGAGGAGCCA 64
 DB |||||
 QY 61 GCGGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGCACCTGCGCA 120
 DB |||||
 QY 65 GCGGTGGCTTCTTCCCTCACTCTCTGAAGTGTCTCTCTGCTGTGCACCTGCGCA 124
 DB |||||
 QY 121 GCCCAGGATTCAGCTCAGGCGCCCTCACTCAGGAGCCCTCTCTCTACCGAATACGAA 180
 DB |||||
 QY 125 GCCCAGGATTCAGCTCAGGCGCCCTCACTCAGGAGCCCTCTCTCTACCGAATACGAA 184
 DB |||||
 QY 181 CGCTTCTTCGCACTGTCTGCTCCAACTCGAAGGACAGACTACCTGCGCTCTCGTGCA 240
 DB |||||
 QY 195 CGCTTCTTCGCACTGTCTGCTCCAACTCGAAGGACAGACTACCTGCGCTCTCGTGCA 244
 DB |||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 14:11:37 ; Search time 7500 Seconds
(without alignments)
9617.572 Million cell updates/sec

Title: US-09-559-013E-23
Perfect score: 1895
Sequence: 1 gttagaggcgtgtgtcc.....tggtgatcttcaaaaaaaaa 1895

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	990	52.2	1037	4	BM554354
2	942.4	49.7	1026	4	BM553910
3	936.2	49.4	1076	4	BM564020
4	928.8	49.0	1074	4	BM563920
5	925.6	48.8	1023	4	BM554310
6	909	48.0	1093	4	BM563837
7	888.8	46.9	1122	4	BM553334
8	861.8	45.5	1012	4	BM554519
9	832.8	43.9	836	4	BM830966
10	828	43.7	891	4	BM520136
11	823.2	43.4	991	4	BM825474
12	799.2	42.2	825	4	BM825274
13	793.6	41.9	823	4	BM828365
14	788	41.6	854	4	BM826371
15	782.8	41.3	827	4	BM820181
16	779.4	41.1	847	4	BM829134
17	773	40.8	909	4	BM827705
18	766.4	40.4	849	4	BM830306
19	764.8	40.4	866	4	BM828510
20	761.6	40.2	779	4	BM829361
21	754.4	39.8	855	4	BM829361
22	752	39.7	843	4	BM831575
23	750.2	39.6	892	6	CD557111
24	749	39.5	829	4	BM825294

25	725.6	38.3	773	4	BM554354
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27	725.2	38.3	919	4	5', mRNA sequence.
28	723.4	38.2	737	4	BM554354
29	722.4	38.1	736	4	BM554354.1 GI:18793882
30	722	38.1	769	4	EST.
31	718.2	37.9	753	4	Homo sapiens (human)
32	717.2	37.8	762	4	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
33	715.8	37.8	793	4	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
34	713	37.6	1029	4	1 (bases 1 to 1037)
35	706.6	37.3	762	4	NIH-MGC http://mgc.mci.nih.gov/.
36	706.2	37.3	741	4	National Institutes of Health, Mammalian Gene Collection (MGC)
37	704.4	37.2	706	4	Unpublished (1999)
38	702.6	37.1	910	4	Contact: Robert Strausberg, Ph.D.
39	699.2	36.9	753	4	Email: cgabbs-r@mail.nih.gov
40	692.8	36.6	768	4	Tissue Procurement: Life Technologies, Inc.
41	687.8	36.3	860	4	cDNA Library Preparation: Life Technologies, Inc.
42	687.4	36.3	689	4	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
43	685.8	36.2	918	6	CD359186 AGENCOURT
44	680.8	35.9	886	6	CD243482 AGENCOURT
45	667	35.2	718	4	CD243482 AGENCOURT

ALIGNMENTS

RESULT 1

BM554354

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

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/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: EcoRV (destroyed); RNA source normal medulla from

anonymous male age 27. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.3 kb, insert size range

0.9-3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 013. Note:

this is a NIH_MGC Library."

ORIGIN

Db 305 GTGCCGATGGTGTCTCTCTCCAACTCCCTTATGCTCCTCTGTTTGAGTCTTTCTGTC 364
Qy 361 CAGTTCACTCACTACCGTTGCTCCACACAGGTCTACTATGCTCCAAAGAGTCTCTGTTCC 420
Db 365 CAGTTCACTCACTACCGTTGCTCCACACAGGTCTACTATGCTCCAAAGAGTCTCTGTTCC 424
Qy 421 CAGCCAGTCTCTATTCTCTCACCTTAACACTCTCAAGGAGATAGAAGCTTCAGCTGAAGTC 480
Db 425 CAGCCAGTCTCTATTCTCTCACCTTAACACTCTCAAGGAGATAGAAGCTTCAGCTGAAGTC 484
Qy 481 TCACCCACACAGATGACCTCCCTCATCTCACCCCACTTCACAGTGAAGAACGCCAGACC 540
Db 485 TCACCCACACAGATGACCTCCCTCATCTCACCCCACTTCACAGTGAAGAACGCCAGACC 544
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Db 545 TTCAGCCTCTGGCTCAGAGGCTCAGCAACAGCTGGAGAGCTCTCAATCTCTCTTG 604
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Db 665 CAGGAGCCGACACAGAAACACAGAGAGGAGGCGCAGAAACAGGAGCAAGAGAG 724
Qy 721 GAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 725 GAACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 784
Qy 781 GTGTCTCAGCTGACAGACACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTCTAAC 840
Db 785 GTGTCTCAGCTGACAGACACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTCTAAC 844
Qy 841 CTTCTCTCTTTGCTCCCGGTACGAGAGTAGAGTCTACTCTCTATGATATGGAGAAC 900
Db 845 CTTCTCTCTTTGCT-CCCGGTACGAGAAATAGAGTCTACTCTATGATATGGAGAAC 903
Qy 901 ATCCAGGAGCTCATTCGATCAGCCAGGAAATAGATGAATGAT--GAAATATATGAG 958
Db 904 ATCCAGGAGCTCATTCGATCAGNCCAGAAATAGATGGAATGAATGGAATATATGAG 963
Qy 959 AGAATCTCTACTGGA-GAAACCAAAACCTTGGCAGCTTCTGAGCTGCCCCACACAGAG 1017
Db 964 AAAATCTCTACTGGAAGAAACCAACCCCTTGGCAGCTTCTGAGCTGCCCCACAGAA 1023
Qy 1018 GCC 1020
Db 1024 GGC 1026

RESULT 3
BM564020
LOCUS
DEFINITION AGENCOURT 6560257 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742040
5' mRNA sequence.
ACCESSION BM564020
VERSION BM564020.1 GI:18811457
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM12759 row: i column: 17
High quality sequence stop: 758.
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/clone="IMAGE:5742040"
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/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 49.4%; Score 936.2; DB 4; Length 1076;
Best Local Similarity 99.0%; Pred. No. 5.7e-223;
Matches 963; Conservative 0; Mismatches 8; Indels 2; Gaps 2;
Qy 22 CGGGAGCGGGCGGATCTTCTCGGCGCATGAGGAAGCCAGCGCTGCTTCTTCCCTCA 81
Db 21 CGGGAGCGGGCGGATCTTCTCGGCGCATGAGGAAGCCAGCGCTGCTTCTTCCCTCA 80
Qy 82 CTCCTGAAGGTGCTGCTCTGCTCTGCACTGCGCAGCCAGGATTGCAATCAGGCTC 141
Db 81 CTCCTGAAGGTGCTGCTCTGCTCTGCACTGCGCAGCCAGGATTGCAATCAGGCTC 140
Qy 142 CCCACTCCAGGCGGCTCTCTCTACCGGATAGGAAGCTTCTTCCGACTGCTGACT 201
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Db 201 CCAACTGGAAGCGAGAGACTACTCTGCTCTCCGTCGCAACCCAGCGCTGCCGGAATCCC 260
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Qy 322 TCCAACTCTCTTATGCTCTGCTGTTGAGTCTTTTCTGCGAGTTCTCACTACCGTTGC 381
Db 321 TCCAACTCTCTTATGCTCTGCTGTTGAGTCTTTTCTGCGAGTTCTCACTACCGTTGC 380
Qy 382 TCCAACTCTCTTATGCTCTGCTGTTGAGTCTTTTCTGCGAGTTCTCACTACCGTTGC 441
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Qy 442 CTTAACTCTCTCAAGGAGATAGAAGCTTCAGCTGAAGTCTCAACCCAGGATGACCTCC 501
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Qy 502 CCCATCTCAACCCACTTTCAGTGACAGAACCGCAGACCTTCAGCCCTGCGCTGAGAGG 561
Db 501 CCCATCTCAACCCACTTTCAGTGACAGAACCGCAGACCTTCAGCCCTGCGCTGAGAGG 560
Qy 562 CTCACCAACAGTGGAGAGCTCTCAATCTCTCTGCTGCTGGAGGCGCAGGAGGCA 621
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Qy 622 GCGCCAGAGCAACAGCAGGAGCAAGAGTGGAGCAGCAGGAGCGGAGCGGACCAAGAACAC 681
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[illegible]

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12759 row: d column: 23

High quality sequence start: 11

High quality sequence stop: 724.

FEATURES

Location/Qualifiers
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/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 48.0%; Score 909; DB 4; Length 1093;
Best Local Similarity 94.2%; Pred. No. 3.7e-216;
Matches 1011; Conservative 0; Mismatches 50; Indels 12; Gaps 6;

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QY 79 TCATCTCTGAAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 138
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DB 201 ACTCCAACTCCGAGGACAGACTACTCTGCGCTCTGCTGCAACCCAGCGTCCGCGAAT 260
QY 259 CCCACACTCTGAGCTGAGCAATATGAAACCAACCGCTTAGTGCCTGATGCTGCTG 318
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DB 561 AGGCTCAGCAACAGCTGAGAGTCTCTCAATCTCTCTCTCTCTCTCTCTCTCT 620
QY 619 CAAGGCCAGGACCAAGCAGGAGCAAGGAGTGGAGCAGCAGGAGGAGGAGGAGGAG 678
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DB 741 AAGCAGGAAGAGGACAGGGGAGCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800
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QY 972 GAGAAACCAAAACCTTCCGAGCTTCTTCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
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RESULT 7
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ACCESSION
  BM553134
VERSION
  BM553134.1 GI:18791598
KEYWORDS
  EST.
SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1122)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: Life Technologies, Inc.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM12761 row: k column: 05
  High quality sequence stop: 707.
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    Site 2: EcoRV (destroyed); RNA source normal medulla from
    anonymous male age 27. Library is oligo-dT primed and
    directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.3 kb, insert size range
    0.9-3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber

```

(Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

ORIGIN

Query Match	46.9%;	Score 888.8;	DB 4;	Length 1122;
Best Local Similarity	93.5%;	Prod. No. 4.2e-211;		
Matches 1025;	Conservative 0;	Mismatches 56;	Indels 15;	Gap8 9;
Qy	1	GTTAGAGCGCGCTTGTGTCTCAACGGGAGCGCGGGCGGATCTTCTCGGGCCATCAGGAAGCCA	60	
Db	25	GTTAGAGCGCGCTTGTGTCTCACGGGACGGGGCGGATCTTCTCGGGCCATCAGGAAGCCA	84	
Qy	61	GCCTGTGGCTTCTTTCCTCTACTCTGAAAGTGTCTGTCTGTGCCTCTGGGCACTGGGCACTGGCGCA	120	
Db	85	GCCTGTGGCTTCTTTCCTCTACTCTGAAAGTGTCTGTCTGTGCCTCTGGGCACTGGGCACTGGCGCA	144	
Qy	121	GCCCAGGATTCGACTCAGGGCCCCACCTCCAGGCGAGCCCTCTCTCTCTCCTACCGAATACGAA	180	
Db	145	GCCCAGGATTCGACTCAGGGCTCCACTCCAGGCGAGCCCTCTCTCTCTCTACCGAATACGAA	204	
Qy	181	CGCTTCTTCGCACTGTGACTCCAACTTGGAAAGCAGAGACTACTGCGCTTCCGTTGCA	240	
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Qy	241	ACCCAGGGCTGCCGGAATCCCACTCGTCCAGCTGGACCAATATGAAACCAACCGGCTTA	300	
Db	265	ACCCAGGGCTGCCGGAATCCCACTCGTCCAGCTGGACCAATATGAAACCAACCGGCTTA	324	
Qy	301	GTGCCGATGGTGTCTGTCTGCTCCAACTCCCTTATGCTCTCTCGTTTGGTCTTTCTTCG	360	
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Qy	361	CAGTTCTACTACCGTTGCTCCAAACACGCTTACTATGTCACAGAGAGTCTCTGTGTTCC	420	
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Qy	421	CAGCCAGTCTCTATTCTCTACCTTAACTCTCAAGGAGATAGAAAGCTTCAGCTGAAATC	480	
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Qy	481	TCACCCACCAAGATGACCTCCCACTCTCACCCCACTTCACAGTGACAGAACCGCAGACC	540	
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Qy	541	TTCCAGCCCTGGCCCTGAGAGCTCAGCAACACGTGGAGAGTCTCTCAATCTCTCTTG	600	
Db	565	TTCCAGTCTCTGGCCCTGAGAGCTCAGCAACACGTGGAGAGTCTCTCAATCTCTCTTG	624	
Qy	601	TCCCTGGAGGCCAGGAGCAAGCCACAGCAGAGCAGCAAGCAGGAGTGGAGCAGCAGG	660	
Db	625	TCCCTGGAGGCCAGGAGCAAGCCACAGCAGAGCAGCAAGCAGGAGTGGAGCAGCAGG	684	
Qy	661	CAGGAGCCGACACAAGAACACAAGCAGGAAGAGGGCGAGAAACAGGAGAGCAAGAGAG	720	
Db	685	CAGGAGCCGACACAAGAACACAAGCAGGAAGAGGGCGAGAAACAGGAGAGCAAGAGAG	744	
Qy	721	GAACA-CGGAAGAGAGGGGAAGCAGGAAGAGGACAGGGG---ACTAAGAGGAGCGGGA	776	
Db	745	GAACAAGAGAGAGGGGAAGCAGGAAGAGGACAGGGGACTANAGGGAGGAGCGGGA	804	
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Qy	954	TGATGA-GAACTCCTACTCGG-AGAAACCAAAACCTCGGAGCTTCTCTGACGCTCCCCCAC	1011	

D	b	984	TGATGAGAACTCCTACTTGAAGAACAACCAAACTGGGAAGCCCTCTCGAGGTGCCCAA	1043
Q	y	1012	ACAGAGCCC-----TTGCTGGTGCTGTGCATTTCGATCGTGGAGAAATACCTGCATCATATAA	1066
D	b	1044	ACAAAGGCCCTTCTTCTGGGGGTTGGGCAATTTCATCGGGAAGAAAACCTGCATTAATAA	1103
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VERSION BM554519.1 GI:18794182				
KEYWORDS EST.				
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ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1. (bases 1 to 1012)				
NIH-MGC http://mgc.nci.nih.gov/.				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: rgs@nih.gov				
Tissue Procurement: Life Technologies, Inc.				
CDNA Library Preparation: Life Technologies, Inc.				
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
DNA Sequencing by: Agencourt Bioscience Corporation				
Clone distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
Plate: LLAM12760 row: p column: 01				
High quality sequence stop: 673.				
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anonymous male age 27. Library is oligo-dT primed and				
directionally cloned [EcoRV site is destroyed upon				
cloning]. Average insert size 1.3 kb, insert size range				
0.9-3 kb. Library is normalized and enriched for				
full-length clones and was constructed by C. Gruber				
(Invitrogen). Research Genetics tracking code 013. Note:				
this is a NIH_MGC Library."				
ORIGIN				
Query Match 45.5%; Score 861.8; DB 4; Length 1012;				
Best Local Similarity 97.0%; Pred. No. 2.3e-204;				
Matches 921; Conservative 0; Mismatches 22; Indels 6; Gaps 4;				
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D	b	63	CATCTCTGAAGGTGCTCTCTCTCCCTCTGGCACTCGCGCAGCCAGGATTCGACTCAGG	122
Q	y	140	CCCCCACTCAGGACGCCCTCTCTCTCTTACCGAATACGAACGGTTCTTCGCACTGCTGA	199

QY	623	CGCCAGACGACACAGCAGGAGCAAGGAGTGGAGCACAGGCAGGAGCCGACACAAGAACAACA	688
Dd	601	CGCCAGAGACGACAAAGCAGGAGCAAGGAGTGGAGCACAGGCAGGAGCCGACACAAGAACAACA	660
QY	683	AGCAGGAAGAGGGGCGAGAAAACAGAAAGCAGCAGCAAGAGAGGAACAGAACAGGAGGGGAAAGC	742
Dd	661	AGCAGGAAGAGGGGCGAGAAAACAGAAAGCAGCAGCAAGAGAGGAACAGAACAGGAGGGGAAAGC	720
QY	743	AGGAAGAAGGACAGGGGACTAAGGAGGGAACGGGAGGCTGTGTCTCAGCTGCAGACAGACT	802
Dd	721	AGGAAGAAGGACAGGGGACTAAGGAGGGAACGGGAGGCTGTGTCTCAGCTGCAGACAGACT	780
QY	803	CAGAGCCCCAGTTTCACCTCTGAATCTCTATCTTCTTAACCCCTTCCTCTTTTGCTCCC	858
Dd	781	CAGAGCCCAAGTTTCACCTCTGAATCTCTATCTTCTTAACCCCTTCCTCTTTTGCTCCC	836
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LOCUS			
DEFINITION			
mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<p>BI520136 891 bp mRNA linear EST 29-AUG-2001 603071275F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5163259 5', mRNA sequence. BI520136 GI:15344928 EST. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 891) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: csapbs@email.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHAM1405 row: e column: 20 High quality sequence stop: 843. Location/Qualifiers 1 . 891 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clones="IMAGE:5163259" /tissue_type="medulla" /lab_host="DH10B" /clone_lib="NIH_MGC_119" /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note this is a NIH_MGC Library."</p>			
FEATURES			
source			
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Query Match 43.7%; Score 328; DB 4; Length 891;			
Best Local Similarity 99.0%; Pred. No. 6.6e-196;			
Matches 875; Conservative 0; Mismatches 5; Indels 4; Gaps 4			
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Dd	5	GTTAGAGCGCGTTGTGTCCACGGAGCGCGGGCGGATCTTCTTCGGCCCATGAGGAAGCCA	64
QY	61	GCCGCTGGCTTCCTTCCTCACTCCTCAAAGGTGTGTCTTCGCTCTGGCACCTGCCGCA	120

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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ORIGIN

Query Match 43.4%; Score 823.2; DB 4; Length 991;
 Best Local Similarity 97.8%; Pred. No. 1.1e-194;
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QY	82	CTCTGAAGTGTCTCTGCTCTGCGACCTGCGCGAGCGCGCGATTCGACTCAGGCC	141
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QY	201	TCCAACTGGAAGCGAGACTACCTGCGTCTCGTGCAACCCAGCGGTGCGGATCC	260
Db	181	TCCAACTGGAAGCGAGACTACCTGCGTCTCGTGCAACCCAGCGGTGCGGATCC	240
QY	261	CACACTGCTCAGCTGGACCAATATGAAACCAACCGCTTAGTGCCGATGCTGCTG	320
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Db	301	CTCAACCTCCCTTATGCTCTGTTTTCAGTCTTTCGCACTTCTATTCCTC	360
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QY	561	GCTCAGCAACAGTGGAGAGCTCCTACATTCCTTGTCTTGGAGGCGGAGGCA	620
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QY	621	AGCGCCAGAGCACAAGCAGGAGCAAGGAGTGGAGCAGGAGGAGCCGACACAGAACA	680
Db	601	AGCGCCAGAGCACAAGCAGGAGCAAGGAGTGGAGCAGGAGGAGCCGACACAGAACA	660
QY	681	CAAGCAGGAGAGGGGCGAGAAACAGGAAGAGCAAGAGGAACAGGAGGAGGAAA	740
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QY	741	GCAGGAAGAAGCA-CAGGGGACTAAGGAGGAGCGGAGGCTGTCTCAGCTGCAGACAG	799
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QY	800	ACTCAGAGCCCAAGTTTCACTCTGAATCTCTA-TCTTCTAACCCCTTCTCTTTT--GCTC	856
Db	781	ACTCAGAGCCCAAGTTTCACTCTGAATCTCTA-TCTTCTAACCCCTTCTCTTTT--GCTC	840
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Db	841	CCCGGTACGAGAGTACTCTCTATGATATGAGGAACA-TCCAGGAGTCA-T	900
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 mRNA sequence.
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 BI825274.1 GI:15936824
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 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11407 row: c column: 19
 High quality sequence stop: 825.
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 /clone="IMAGE:5163978"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

REFERENCE

1. (bases 1 to 827)
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11405 row: j column: 07
 High quality sequence stop: 826.

FEATURES

source

1. 827
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5163366"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 41.3%; Score 782.8; DB 4; Length 827;
 Best Local Similarity 98.3%; Pred. No. 1.3e-184;
 Matches 812; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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 DB 1 TGCATTCGATCGTGGAGAAATACCTGCATCAATACCCACAGCCCAAGCCCTGGAGTAC 60

QY 1093 ATGGAGGAGAGATCCCTGGTTTCGGGAAGTCGGTCTGTGACAGCCTTGGGCGGACAC 1152
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QY 1153 ATGTCTACCTGTGCCCTCTGTGACTTCTGCTTGAAGCTGGAGCGCCACTCAGAG 1212
 DB 121 ATGTCTACCTGTGCCCTCTGTGACTTCTGCTTGAAGCTGGAGCGCCACTCAGAG 180

QY 1213 GCCAGCCTGCAGCGCAACAAATCGACACCTCCCAAGACTCCCTTTGTGAGCCCTTG 1272
 DB 181 GCCAGCCTGCAGCGCAACAAATCGACACCTCCCAAGACTCCCTTTGTGAGCCCTTG 240

QY 1273 CTTGCTCCCAAGCCTGTCCATFCGCAACCAAGTAGGGTCCCAAGATCAGGCCGCTTT 1332
 DB 241 CTTGCTCCCAAGCCTGTCCATFCGCAACCAAGTAGGGTCCCAAGATCAGGCCGCTTT 300

QY 1333 TAGGGCTGGATTGTACGGTGGCTCCACATGGACTTCTGGTGTCCCGGCTTGCACG 1392
 DB 301 TAGGGCTGGATTGTACGGTGGCTCCACATGGACTTCTGGTGTCCCGGCTTGCACG 360

QY 1393 AAAGGCTGTGAAGATCTCCGAGTCTCTGGTGGCTCCAGACTGAGTTCCTTAGCTCCAG 1452
 DB 361 AAAGGCTGTGAAGATCTCCGAGTCTCTGGTGGCTCCAGACTGAGTTCCTTAGCTCCAG 420

QY 1453 GATGGGGATTTCCCTACCAAGATTTGTGACAGACTATATCCAGTACCCAACTACTGT 1512
 DB 421 GATGGGGATTTCCCTACCAAGATTTGTGACAGACTATATCCAGTACCCAACTACTGT 480

QY 1513 TCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGCCCGCATGAGA 1572

DB 481 TCCTTCAAAAGCCAGCAGTGTCTGATGAGAAACCGCAATCGGAGGTGCCCGCATGAGA 540
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 DB 720 TCAGGCTGCCCTTCTGGGTCTGTTACTCGGCCCTTACTCACAATTTCTTTGGTTGGAGC 779
 QY 1813 AACAGTCCAGAGAGGGCCACGGTGGAGCTGGCCCTCTCTTAAAA 1858
 DB 780 AACAGTCCAGAGAGAGGG--CACGGTGGAGCTGGCCCTCTCTTAAAGA 824

Search completed: March 7, 2005, 19:45:25

Job time : 7505 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 08:35:27 ; Search time 8236 Seconds
(without alignments)
11148.936 Million cell updates/sec

Title: US-09-559-013E-23

Perfect score: 1895
Sequence: 1 gtagagcgcgctgtgtcc.....tgttgatctcaaaaaaa 1895

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1890.2	99.7	1912	6	BD268022
2	1888.8	99.7	1899	9	BC033010
3	1886	98.5	1886	9	AB051833
4	1856.4	98.0	1899	6	BD192303
5	1811.2	95.6	1892	6	BD136402
6	1258	66.4	1813	4	PIGACRSN
7	1128.2	59.5	1841	4	MUSSP32A
8	1125.4	59.4	1880	10	GPIACRSN
9	937.6	49.5	964	6	BD139445
10	768.4	40.5	2289	6	CQ722423
11	612.2	32.3	1553	10	MUSSP32B
12	610.6	32.2	1524	10	BC011079
13	604.2	31.9	1284	10	BC079212
14	471.8	24.9	56520	9	AC135892
15	471.8	24.9	245880	2	AC079387
16	339	17.9	516	9	HUMWP42A04
17	337.2	17.8	522	6	BD179034
18	329.8	17.4	507	6	BD179252
19	282.4	14.9	308	6	BD060281

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21	274.2	14.5	166392	10	AC134529	AC134529 Mus muscu
22	271.4	14.3	391	11	G23540	G23540 human STS W
23	269.6	14.2	658	10	BC061122	BC061122 Mus muscu
24	258.8	13.7	316	6	AR415759	AR415759 Sequence
25	258.8	13.7	316	6	AX972593	AX972593 Sequence
26	258.8	13.7	316	6	BD111312	BD111312 EST and e
27	124.4	6.6	128	6	AX968632	AX968632 Sequence
28	124.4	6.6	128	6	BD073650	BD073650 5'EST of
29	106.8	5.6	67573	2	AC122760	AC122760 Mus muscu
30	87.4	4.6	168365	10	AC131653	AC131653 Mus muscu
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ALIGNMENTS

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ACCESSION	BD268022	BD268022.1 GI:33077790			
VERSION	BD268022	BD268022.1 GI:33077790			
KEYWORDS	JP 2002522081-A/10.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bandman, O., Hillman, J.L., Baughn, M.R., Azimzai, Y., Guegler, K.J.,				
AUTHORS	1 (bases 1 to 1912)				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	Proteases and associated proteins				
JOURNAL	Patent: JP 2002522081-A 10 23-JUL-2002;				
COMMENT	INCYTE PHARMACEUTICALS INC				
OS	Homo sapiens (human)				
PN	JP 2002522081-A/10				
PD	23-JUL-2002				
PF	06-AUG-1999 JP 2000565144				
PR	10-AUG-1998 US 60/096114, 11-FEB-1999 US 60/119768 PI				
OLGA	BANDMAN, JENNIFER L, HILLMAN, MARIAH R, BAUGHN, YALDA AZIMZAI, PI				
KARL, J	GUEGLER, NELL C CORLEY, HENRY YUE, TOM Y TANG, ROOBA REDDY, PI				
CHANDRA	PATTERSON, JANICE AU YOUNG, LEO L SHIH, DYUNG AINA M LU PC				
C12N15/09	,A61K38/00,A61K45/00,A61P37/00,A61P43/00,C07K16/40, PC				
C12N1/15	, PC				
PC	C12N1/19,C12N1/21,C12N5/10,C12N9/48,C12P21/08,C12Q1/68,C12N15/				
PC	00,C12N5/00,				
PC	A61K37/02				
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 Db 1697 GCTGAGCTGATATCTGACCAACCCAGGCCAAGCTGCTGATTTGATTTGAG 1756
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 Db 1877 TGACTTTACATAAATGTTGATCTTCAAAAAA 1911

RESULT 2
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 DEFINITION IMAGE:482765), complete cds.
 ACCESSION BC03010
 VERSION BC03010.2 GI:34783873
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1899)

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 Db 1081 TGGAGTACATGAGAGAGAGATCTTGGTTTCGGAGTGGTCTGTGAAGCTTGGG 1140
 QY 1144 CGCGACACATGCTTACTGCTGCTGTGATCTTGTCTCTTGAAGCTGAGAGAGTGC 1203
 Db 1141 CGCGACACATGCTTACTGCTGCTGTGATCTTGTCTCTTGAAGCTGAGAGAGTGC 1200
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RESULT 3
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DEFINITION Homo sapiens mRNA for proacrosin binding protein sp32 precursor,
 complete cds.
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 VERSION AB051833.1 GI:13366085
 KEYWORDS SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Ono, T., Kurashige, T., Harada, N., Noguchi, Y., Saita, T., Niihara, N.,
 Aoe, M., Nakamura, S., Higashi, T., Hiraki, A., Wada, H., Kunio, H.,
 Old, L.J. and Nakayama, E.
 Identification of proacrosin binding protein sp32 precursor as a
 human cancer/testis antigen
 Proc. Natl. Acad. Sci. U.S.A. 98 (6), 3282-3287 (2001)
 JOURNAL MEDLINE
 PUBMED 21145836
 REFERENCE 2 (bases 1 to 1886)
 AUTHORS Ono, T. and Nakayama, E.
 TITLE Direct Submission
 JOURNAL Submitted (27-NOV-2000) Toshiro Ono, Okayama University Medical
 School, Department of Immunology, 2-5-1 Shikata-cho, Okayama,
 Okayama 700-8558, Japan (E-mail: onotomed@okayama-u.ac.jp,
 Tel:81-86-235-7192, Fax:81-86-235-7193)
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CDS

gene

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 VERSION BD136402.1 GI:23231347
 KEYWORDS JP 2002506627-A/89.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1892)
AUTHORS Ruben,S.M., Ni,J., Rosen,C.A., Yu,G.L., Young,P.E., Fen,P.,
Soppet,D.R., Wei,Y.F., Endress,G.A., Duan,R.D., Kyaw,H., Ebner,R.,
Lafleur,D.W., Olsen,H.S., Shi,Y. and Moore,P.A.
TITLE 95 human secretory proteins
JOURNAL Patent: JP 2002506627-A 89 05-MAR-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Homo sapiens (human)
PN JP 2002506627-A/89
PD 05-MAR-2002
PR 18-MAR-1998 JP 2000536733
PR 19-MAR-1998 US 60/078566,19-MAR-1998 US 60/078576 PR
19-MAR-1998 US 60/078573,19-MAR-1998 US 60/078574 PR
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ACCESSION	U15200			

VERSION	D16200.1	GI:475020
KEYWORDS	acrosin.	
SOURCE	Sus scrofa	(pig)
ORGANISM	Sus scrofa	

REFERENCE
AUTHORS

Ichimura, I., & Saito, Y. (1983).
1 (bases 1 to 1813)
Baba, T., Nida, Y., Michikawa, Y., Kashihara, S.
Kodaira, K.

TITLE	Ishenakka, M., Konno, N., Gerton, G. L. and Arii, Y. An acrosomal protein, sp32, in mammalian sperm is a binding protein specific for two proactosins and an actrosin intermediate
JOURNAL	J. Biol. Chem. 269 (13), 10133-10140 (1994)
MEDLINE	94193559

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1813)
Baba,T.
Direct Submission
Submitted (06-MAY-1993) Tadashi Baba
University of Tsukuba

City, Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)
Location/Qualifiers
1. .1813

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361 GGTGCTCCAGCCTGTCTTAATCTCTCACTTAACCTCTTCAGAGAGTGTGACACTTCT 420

473 CTGAAGTTCACCCACACGATGACTCCCCCATTCACCCCACTTCAACAGTGACAGAAC 532

421. CTGAAGTGGGATCAACAGATGACTCCCCGGTGTCTCTCCACATCAACGCCACAGGGC 480

481 GACAGGCTTCCAGCCCTGGCCGAGCGGCTCAACACACACAGTGGAGGAGCTGTACAAT 540

541 CCTCTTCTCCCTGGCGCGCCAGAGCAAGGCCAGAGCAACAAGCA-----GG 588

653 AGCAGAGCGAGAGCCGACACACAGAACACAAAGCAGAGAGGGGCGAGAAACAGGAAAGAC 712
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588 AGCAGAGCGAGAGCCGACACACAGAACACAAAGCAGAGAGGGGCGAGAAACAGGAAAGAC 712
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713 AAGGAAGGAAACAGGAAAGAGAGGGAAAACAGCAAGAGAAGAGCATTAAAGGAGGC 648
 DY LLLLLLLLLL LLLLLLLLLL LLLLLLLLLL LLLLLLLLLL LLLLLLLLLL LLLLLLLLLL
 209 AGAACCAAACACAGGAGCAAGAGGGCCAGAGGCCACMACAGAGACGAGGGGGCAGGAGCAGCAAGCAAGAC

649 AAGAGGAGGAGCAGAGGAGGAGGAGGAGAGAGAGCAGGCGACCCGAGAGTCC 708

709 TGGAGGCAATGCTGGGCTACAGGCAAGCTCAGAGCCCAAGTTCACCTGTAATTGTCT 768

833 CTTCGACCCCTTCTTTTGCTCCCGGGTAGAGAAGTACTCCTATGATAA 892
769 CTTCCGAACCCCTTCTTTTGCTCCCGGGTAGAGAAGTACTCCTATGATAA

893 TGAGAACATCCAGAGCTCATTCGATCAGGCCAAGAAATGATGAATGAATGAATAT 952
TGCACCGGGGTGGCGGAGGTGAGTGACCCCCCATGATGA 828

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 Db 370 ACCAGCTCTACTATGAGTGTGAGAGTCTGTGTGCTCCAGGCTGTCTATCTGTCACTA 445
 QY 446 ACACCTCAAGAGATAGAGTCTGAGTGAAGTCTCACTCCACGATGACCTCCCA 505
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 QY 506 TCTCACTCCCTATGAGTGTGAGAGTCTGTGTGCTCCAGGCTGTCTATCTGTCACTA 565
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 QY 566 GCAACAACTGAGAGTCTGAGTGAAGTCTCACTCCACGATGACCTCCCA 625
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 QY 686 AGAAGAGAGGAG 742
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 QY 743 AGAAG 802
 Db 727 AGAAG 786
 QY 803 CAG 862
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 QY 863 TAG 922
 Db 847 TCCGAG 906
 QY 923 CCCAG 982
 Db 907 CCCAG 960
 QY 983 ACCCTGAG 1042
 Db 961 GCACTGAG 1020
 QY 1043 TCGTGAAG 1102
 Db 1021 TTAATGAAG 1080
 QY 1103 AGATCTCTGAG 1162
 Db 1081 AGATCTCTGAG 1140
 QY 1163 GTGCTCTCTGAG 1222
 Db 1141 GTGCTCTCTGAG 1200
 QY 1223 AGCGGCAACATGAG 1282
 Db 1201 TGGGCGAAG 1260
 QY 1283 AGAGCGCTGTGAG 1342
 Db 1261 AGAGCGATATGAG 1320
 QY 1343 ATTGTGAG 1402
 Db 1321 AATGTGAG 1380

QY 1403 AAGATTCGAGTCTGAG 1462
 Db 1381 AAGATTCGAGTCTGAG 1440
 QY 1463 TCCCTCAAGAGATTTGAG 1522
 Db 1441 TCCCTCAAGAGATTTGAG 1500
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 QY 1703 CCCAG 1762
 Db 1681 CCCAG 1740
 QY 1763 CCTTCTGAGTCTGAG 1822
 Db 1741 CCTTCTGAGTCTGAG 1800
 QY 1823 GAG 1857
 Db 1801 GAG 1835

RESULT 8
 LOCUS GPIACRSN 1880 bp mRNA linear ROD 28-JAN-2003
 DEFINITION Cavia porcellus mRNA for sp32, complete cds.
 ACCESSION D16203
 VERSION D16203.1 GI:474969
 KEYWORDS
 SOURCE Cavia porcellus (domestic guinea pig)
 ORGANISM Cavia porcellus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Hystriognathia; Caviidae; Cavia.
 REFERENCE 1
 Baba, T., Nida, Y., Michikawa, Y., Kashiwabara, S., Kodaira, K.,
 Takenaka, M., Kohno, N., Gerton, G.L. and Arai, Y.,
 An acrosomal protein, sp32, in mammalian sperm is a binding protein
 specific for two proacrosins and an acrosin intermediate
 J. Biol. Chem. 269 (13), 10133-10140 (1994)
 PUBMED 814514
 REFERENCE 2 (bases 1 to 1880)
 AUTHORS Baba, T.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1993) Tadashi Baba, University of Tsukuba,
 Institute of Applied Biochemistry, Tennohdai 1-1-1, Tsukuba, Science
 City, Ibaraki 305, Japan (Tel:81-298-53-6632, Fax:81-298-53-6632)
 FEATURES
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sig_peptide
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3'UTR
polya_signal
Origin

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Query Match	59.4%;	Score 1125.4;	DB 10;	Length 1880;
Best Local Similarity	80.2%;	Pred. No. 1.2e-302;		
Matches 1377;	Conservative 0;	Mismatches 321;	Indels 19;	Gaps 4

QY	20	CAGGGAGCGGGGCGGATCTTCTCCGGCCATGAGGAGCCAGCCGCTGAGCTTCTCTTCCCT	79
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QY	80	CATCTCTGAAGGTGTGCTCTCTGCTCTTGCGCACCTGGCCAGGCCAGGATTTGACTCAGG	139
Db	81	CATGCTGAGGGGTGTGCTCTCTGCTCTTGCGGACCTGCTCTGCGCAGGACTCTCCCTGG	140
QY	140	CCCCACCTCCAGGGAGCCCTCTCTCTCTCTAACCAGTAAGAAAGCTTTCTTTCGACTGCTGA	199
Db	141	CTCTTACTCCAGGAGATGCCCTCTCTCTCCACCGAATAGAGGGCTTCTTTCGCCCTGCTCA	200
QY	200	CTTCAACTTGGAGAGCAGAGACTACCTGCGCTGCTCCGTGCAACCCAGCGATCCGGAAATC	259
Db	201	CCCCACTTGGAAAGGACAGAGACCACTTCGCTCGGCTTCCGAGCTTACCAAGGCTTGCAGAAAC	260
QY	260	CCACACTCTGTCAGCTGGACCAATATGAAAAACAAGCTTATGTGCCCCATGTGTCTGTCT	319
Db	261	CCACCATCTGTCAAGCTGGACCAATATGAAACACAGGCTGTGTGCCCCAGCGCGTGTCT	320
QY	320	GCTCCAACTTCCCTTTATGCTCTCTGCTTGTGAGTCTTTCTGCCAGTTCACTACCGTT	379
Db	321	GCTCCGACCTTCCCTTTATGCTCTCTGCTTGTGAGTCTTTCTGCCAGTTCTCAGTACCGCT	380
QY	380	GCTCCAAACCAAGTCTATCTATGSCCAAGAAAGTCTGTCTTCCAGGCACTCTCATTTCTCT	439
Db	381	GCTCCAAACCAAGTCTATCTATGSCCAAGAAAGTCTGTCTTCCAGGCACTCTCATTTCTCT	440
QY	440	CACCTTAACTCTCTCAAGGAGATAGAAAGTTTACGCTGAAGTCTCAACCAACCAAGTACTT	499
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QY	500	CCCCCATCTCAACCCCACTTCAAGTGAAGAAAGCCAGACCTTCCAGCCCTGACCTTGAGA	559
Db	501	CACCCGTCACTCCCACTCAATCAAAAGCAAGAGCGCAAGTCTTCCAGGCTGTGCTTGAGC	560
QY	560	GGCTCAGCAACAAGTGAAGAGTCTCTTCAATCTCTTGTCTCTGGAAGGCCAGAGCC	619
Db	561	GGCTCAGCAACAAGTGAAGAGTCTCTTCAATCTCTTGTCTCTGGAAGGCCAGAGCC	620
QY	620	AAGGCGCAGAGCAACAAGGAGGAGGA---GTGAGACACAGGACAGAGCCGACACAG	676
Db	621	AAGGCGCTGTGCTATTAAGCAGGAGCAAGGACAGAGCACAACAAGAGATTCGACCCAGG	680
QY	677	AACAACAAGCAGGAAGAGGGGCAAGAAACAGAAAGCAAGAAAGAGGAACAGGAAGAGAGG	736
Db	681	AGCAACAAGCAGGAAGATGATGGGCAAGAGCAAGAAAGACAGGAAGAAAGCAAGAGAGAGG	740
QY	737	GAAAACAGGAAGAGGACAGGGGACTTAAGGA-----GGAGCGGAGGCTGTGTCTAGC	790

Db	741	GGAAACAGAAAGAGGGCCAGAGTGTAAAGACATGCTGGGCGAGGGTGGGCGAGGGCCGGCC	800
QY	791	TGCAGACAGACTCAGAGCCCAAGTTTCACTCTGAATCTCTATCTTTACCTCTCTCTT	850
Db	801	TGCGGATATGGCTCCAGAGCCAAAGCCACAGTCCCTCTCTGCTTCCGACCTCTCACTCT	860
QY	851	TTTGCCCCGGGGTTCAGAAAGTAGGTCTACTCCATATATTAAGAAACATCCAGAGAC	910
Db	861	TCACTGCCCGGGGTCCGAACGTGAGCTGGCTCCATATATATGAAGAAATATCCAGAGAC	920
QY	911	TCATTCGATCAGCCCGAGAAATAGATGAATGAATGAATATATATATGAGAACTCTCACT	970
Db	921	TCATTCGATCAGCCCGAGAAATAGAGAAATG-----TACAGAGAGATGCTCACT	971
QY	971	GGAGAAACCAAAACCTTGCGAGCTTCTTGCGAGCTGCCCAACAGAGGCTTGTGCTGTGC	103
Db	972	GGAGAGGCGCAAAACCAAGCGAGCTCTTGCGAGCTGCCCATATAGAGAGGCTTGTGCTGTGC	103
QY	1031	TGTGTATTTGATCGTGTGAAGATACCTGCACTATACCCCAAGCCAAAGCCTGTGAAGT	109
Db	1032	TGTGTATTTGATCGTGTGTGAAGACGTGTGTATGACCCCTCGGCAAGGCTGTGAAGT	109
QY	1091	ACATGAGAGAGAGATCTTGTGTTTCGGGAAGTGGGTGTGTGTGACGCTTGTGGGCGGCGAC	115
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QY	1151	ACATGTCTACCTGTGACCTCTGTGTGACCTTGTGCTCTCTTGAAGCTGTGAGAGTGTGCACTGAG	121
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QY	1211	AGGCGAGCTGTGAGCGGCGACATATGCGACACTTCCACAACTCTTGTGTGACGCTCT	127
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QY	1271	TGCTTGGCTCCCGACAGGCTGTGCATTCGCGCAACGAGTAGGGTCCCGAAATCAGGCGCT	133
Db	1272	TGCTTCAGGCGCGACCAATGTGCATGTGCGACCCAGCGGGACCTCGGAATCTGTGCGCT	133
QY	1331	TTTACCGGCTGGATTGTATCGGTGGGCTCCACATGACCTTGTGTGTGCTCCGCGCTTGTGCA	139
Db	1332	TTTACCGGTTATGATGTATACGCTGGGCTCCGCAATGAAATTTGTGTGTGCCGCGTGGCA	139
QY	1391	CGAAAGCTGTGAAGATGTCCGAGTCTTGTGGGTGCTTCAAGCTGTGATTCCTTAGCTTCC	145
Db	1392	CAAGGCGCTGTGAAGACATCCGGGCTTCCAGCTGGCTTCCAGACGAGGTTCCTCAGCTTCC	145
QY	1451	AGGATGGGGATTTCCCTACCAAGAAATTGTGTGACAGACTATATCAGTACCCAACTA	151
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QY	1511	GTTCCTTCAAAAGCCAGCAGTGTCTGATGTGAAGAAACCGCAATCGAGAGGTGTCCGCACTGA	157
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QY	1571	GATGTCTGTGAGATGTGAACCTTACAGTGTGCTGAGCCTTGTGCAAAAGTGAAGACGTTGTGC	163
Db	1572	GATGTCTGTGAGATGTGAACCTTACAGTGTGCTGAGCCTTGTGCAAAAGTGAAGACGTTGTGC	163
QY	1631	TTTGAATGAGCAGAGATTTACAGCACTTGAATCTTGAAGCACTTGTGGAATGAGACTGGCTCT	169
Db	1632	TTTGAATGAGCAGAGATTTAGCACTTGTGCTTGAAGCGCTTGTGGAATGAGATGG-GTCC	169
QY	1691	ATTCTGCCACACCCAGCCCAACTGTGCCCACTTCT	1727
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RESULT 9			
BD139445	BD139445	964 bp	DNA
LOCUS	BD139445		linear
DEFINITION	Extended cDNA of secretory protein.		
ACCESSION	BD139445		
VERSION	BD139445.1	GI:23234390	PAT 18-SEP-2007

LOCUS	BD139445	964 bp	DNA	PAT 18-SEP-2002
DEFINITION	Extended cDNA of secretory protein.			
ACCESSION	BD139445			
VERSION	BD139445.1	GI:23234390		

KEYWORDS JP 2002508182-A/197.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 964)
AUTHORS Bougueleret, L., Duclet, A. and Edwards, J.B.D.M.
TITLE Extended cDNA of secretory protein
JOURNAL Patent: JP 2002508182-A 197 19-MAR-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002508182-A/197
PD 19-MAR-2002
PF 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUQUELERET, AYMERIC DUCLET, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21
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Von Heljne matrix
CC score 8.5
CC seq LKVLLEPLAPAA/OD
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ORIGIN

Query Match 49.5%; Score 937.6; DB 6; Length 964;
Best Local Similarity 99.3%; Pred. No. 3,1e-250;
Matches 948; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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62 GGGCGGATCTTCTCCGGCCATGAGAACCGCCGCTGCTCTTCTCTCTCACTCTGAA 121
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122 AGGCAAGCCCTCTCTCTCTCAAGAAATGAAAGCTTTCTGCACTGCTGAACTGCA 181
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Db 482 CACCCCACTTCAAGTGAAGCAAGCCGACACCTTCCAGCCTTGCTGAGAGGCTCAGCA 541
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Qy 629 AGCACAAGCAG 688
Db 602 AGCACAAGCAG 661
Qy 689 AAG 748
Db 662 AAG 721
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RESULT 10
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LOCUS CQ722423
DEFINITION Sequence 8357 from Patent WO02068579.
ACCESSION CQ722423
VERSION CQ722423.1 GI:42283280
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE K1s, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 8357 06-SEP-2002;
PB Corporation (NY) (US)
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ORIGIN

Query Match 40.5%; Score 768.4; DB 6; Length 2299;
Best Local Similarity 99.9%; Pred. No. 6.5e-203;
Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	1088	AGTACATGAGAGAGAGAGATCTCTGGTTTCGGGAAGTCGGTCTGTGACAGCCTTGAGCGGC	1147
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QY	1148	GACACATGCTTAACCTGTGACCTCTGTGACTTCTGTCCTTGAAGCTGGAGAGTGCACCT	1207
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QY	1328	GCTTTTACGGGCTGGATTGTGATCGGTGGGCTTCCACATGGAATTCTTGATGTGGCCGGCTTG	1387
Db	896	GCTTTTACGGGCTGGATTGTGATCGGTGGGCTTCCACATGGAATTCTTGATGTGGCCGGCTTG	955
QY	1388	CCACGAAAGGCTGTGAGATGTCGAGATCTCTGGGTGGCTCCAGACTGAGTTCTTTAGCT	1447
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RESULT 13
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 DEFINITION Rattus norvegicus cDNA clone MGC:94274 IMAGE:7131828, complete cds.
 ACCESSION BC079212
 VERSION BC079212.1 GI:50925776
 KEYWORDS MGC.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1284)
 Struhsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Stenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scapleton, M., Soares, M.B., Bernaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Lonnellano, N.A., Peters, G.J.,
 Abramson, R.D., Mulhally, S.J., Bosak, S.A., McKean, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahy, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Buterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalins, D.E.,
 Schmechel, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 2 (bases 1 to 1284)
 DIRECTOR MGC Project.
 DIRECTOR MGC Project.
 DIRECTOR MGC Project.
 Submitted (02-AUG-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Howard Jacobs
 CDNA Library Preparation: Express Genomics
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMLI)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.ahgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

REMARK
 COMMENT
 Cloning distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILMLI at: <http://image.llnl.gov>
 Series: IRAP Plate: 184 Row: m Column: 7
 This clone was selected for full length sequencing because it
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 Location/Qualifiers

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ORIGIN

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VERSION
KEYWORDS HTG; HTGS PHAS1.
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
2 (bases 1 to 245880)
Worley, K.C.
Direct Submission
Submitted (01-SEP-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On or before Sep 1, 2000 this sequence version replaced gi:4589937,
gi:4926836, gi:4589938.
Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: J-11
Center clone name: RP4-761J14, RP11-433J06
Sequencing statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodypy: 92% of reads
Chemistry: Dye-terminator Big Dye: 7% of reads
Assembly program: Phrap; version 0.990329

Consensus quality: 214565 bases at least Q40
Consensus quality: 230283 bases at least Q30
Consensus quality: 240000 bases at least Q20
Estimated insert size: 29807; agarose-fp estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of 42 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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FEATURES

source

ORIGIN

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DB 65272 GTT 65270

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Job time : 8243 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2005, 22:38:33 ; Search time 338 Seconds
(without alignments)
9173.800 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 107	18	0.9	378	4	US-09-513-999C-21497	Sequence 21407, A	C 180	18	0.9	80706	4	US-09-949-016-15347	Sequence 15347, A
C 108	18	0.9	415	4	US-09-621-976-1691	Sequence 1691, A	C 181	18	0.9	81819	4	US-09-949-016-15661	Sequence 15661, A
C 109	18	0.9	425	4	US-09-621-976-1691	Sequence 1691, A	C 182	18	0.9	81819	4	US-09-949-016-15662	Sequence 15662, A
C 110	18	0.9	454	4	US-09-621-976-1691	Sequence 1691, A	C 183	18	0.9	82125	4	US-09-949-016-13517	Sequence 13517, A
C 111	18	0.9	478	4	US-09-621-976-1691	Sequence 1691, A	C 184	18	0.9	82125	4	US-09-949-016-13518	Sequence 13518, A
C 112	18	0.9	509	4	US-09-621-976-1691	Sequence 1691, A	C 185	18	0.9	86936	4	US-09-949-016-15344	Sequence 15344, A
C 113	18	0.9	509	4	US-09-621-976-1691	Sequence 1691, A	C 186	18	0.9	86936	4	US-09-949-016-15345	Sequence 15345, A
C 114	18	0.9	550	4	US-09-918-686-112	Sequence 2943, Ap	C 187	18	0.9	87030	4	US-09-949-016-15361	Sequence 15361, A
C 115	18	0.9	601	4	US-09-949-016-29140	Sequence 12, Appl	C 188	18	0.9	87352	4	US-09-949-016-12703	Sequence 12053, A
C 116	18	0.9	601	4	US-09-949-016-11095	Sequence 29140, A	C 189	18	0.9	87352	4	US-09-949-016-12703	Sequence 12703, A
C 117	18	0.9	601	4	US-09-949-016-11095	Sequence 41909, A	C 190	18	0.9	87352	4	US-09-949-016-15632	Sequence 15632, A
C 118	18	0.9	601	4	US-09-949-016-82981	Sequence 82981, A	C 191	18	0.9	87352	4	US-09-949-016-15633	Sequence 15633, A
C 119	18	0.9	601	4	US-09-949-016-168265	Sequence 168265, A	C 192	18	0.9	87352	4	US-09-949-016-15633	Sequence 15633, A
C 120	18	0.9	601	4	US-09-949-016-168265	Sequence 168265, A	C 193	18	0.9	87352	4	US-09-949-016-15633	Sequence 15633, A
C 121	18	0.9	601	4	US-09-949-016-172218	Sequence 172218, A	C 194	18	0.9	87352	4	US-09-949-016-15633	Sequence 15633, A
C 122	18	0.9	611	4	US-09-949-016-172219	Sequence 172219, A	C 195	18	0.9	91559	4	US-09-949-016-12881	Sequence 12881, A
C 123	18	0.9	951	4	US-09-976-594-111	Sequence 1591, Ap	C 200	18	0.9	92139	4	US-09-949-016-13701	Sequence 13701, A
C 124	18	0.9	960	3	US-08-556-419-9	Sequence 111, App	C 201	18	0.9	92139	4	US-09-949-016-13701	Sequence 13701, A
C 125	18	0.9	1113	4	US-09-252-991A-4148	Sequence 9, Appl	C 202	18	0.9	94830	4	US-09-949-016-12414	Sequence 12414, A
C 126	18	0.9	1238	3	US-09-397-787-265	Sequence 4148, Ap	C 203	18	0.9	94830	4	US-09-949-016-12414	Sequence 12414, A
C 127	18	0.9	1250	4	US-09-370-767-25511	Sequence 266, App	C 204	18	0.9	95648	4	US-09-949-016-16336	Sequence 16336, A
C 128	18	0.9	1302	4	US-09-252-991A-4458	Sequence 25511, A	C 205	18	0.9	95648	4	US-09-949-016-16336	Sequence 16336, A
C 129	18	0.9	1314	4	US-09-252-991A-4458	Sequence 4458, Ap	C 206	18	0.9	95648	4	US-09-949-016-16336	Sequence 16336, A
C 130	18	0.9	1326	2	US-09-902-540-186	Sequence 4290, Ap	C 207	18	0.9	99370	4	US-09-949-016-15403	Sequence 15403, A
C 131	18	0.9	1326	2	US-09-902-540-186	Sequence 186, App	C 208	18	0.9	99370	4	US-09-949-016-15403	Sequence 15403, A
C 132	18	0.9	1326	2	US-09-902-540-186	Sequence 2, Appl	C 209	18	0.9	100877	4	US-09-949-016-17540	Sequence 17540, A
C 133	18	0.9	1330	4	US-09-270-767-10159	Sequence 2, Appl	C 210	18	0.9	100877	4	US-09-949-016-17540	Sequence 17540, A
C 134	18	0.9	1347	4	US-09-620-312D-381	Sequence 10159, A	C 211	18	0.9	101472	4	US-09-949-016-15861	Sequence 15861, A
C 135	18	0.9	2344	3	US-08-416-581B-2	Sequence 381, App	C 212	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 136	18	0.9	2344	3	US-09-526-542-1	Sequence 2, Appl	C 213	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 137	18	0.9	2787	1	US-08-416-581B-3	Sequence 1, Appl	C 214	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 138	18	0.9	2787	1	US-08-416-581B-4	Sequence 3, Appl	C 215	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 139	18	0.9	2787	1	US-08-416-581B-4	Sequence 4, Appl	C 216	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 140	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 217	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 141	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 218	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 142	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 219	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 143	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 220	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 144	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 221	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 145	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 222	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 146	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 223	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 147	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 224	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 148	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 225	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 149	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 226	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 150	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 227	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 151	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 228	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 152	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 229	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 153	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 230	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 154	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 231	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 155	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 232	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 156	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 233	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 157	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 234	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 158	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 235	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 159	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 236	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 160	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 237	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 161	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 238	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 162	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 239	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 163	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 240	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 164	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 241	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 165	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 242	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 166	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 243	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 167	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 244	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 168	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 245	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 169	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 246	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 170	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 247	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 171	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 248	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 172	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 249	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A
C 173	18	0.9	2787	1	US-08-416-581B-4	Sequence 5, Appl	C 250	18	0.9	102500	4	US-09-949-016-15861	Sequence 15861, A

247	18	0.9	156950	4	US-09-949-016-15946	Sequence 15946, A	C 320	17	0.9	483	4	US-09-902-540-3490	Sequence 3490, Ap
C 248	18	0.9	152841	4	US-09-949-016-13753	Sequence 13753, A	C 321	17	0.9	492	4	US-09-621-576-2589	Sequence 2589, Ap
C 249	18	0.9	168104	4	US-09-949-016-12026	Sequence 12026, A	C 322	17	0.9	531	2	US-08-809-185-1	Sequence 1, Appl1
C 250	18	0.9	168105	4	US-09-949-016-16554	Sequence 16554, A	C 323	17	0.9	534	3	US-09-000-630C-26	Sequence 26, Appl
251	18	0.9	168174	4	US-10-071-411A-63	Sequence 63, Appl	C 324	17	0.9	534	3	US-08-882-730C-24	Sequence 24, Appl
252	18	0.9	168273	4	US-10-071-411A-2	Sequence 2, Appl1	C 325	17	0.9	534	3	US-08-862-730C-26	Sequence 26, Appl
253	18	0.9	168394	4	US-09-949-016-13002	Sequence 13002, A	C 326	17	0.9	534	3	US-08-862-730C-26	Sequence 26, Appl
C 254	18	0.9	168575	3	US-09-426-290-1	Sequence 1, Appl1	C 327	17	0.9	534	3	US-09-016-434-1221	Sequence 1221, Ap
C 255	18	0.9	152326	4	US-09-949-016-14353	Sequence 14353, A	C 328	17	0.9	543	1	US-08-422-655-1	Sequence 1, Appl1
C 256	18	0.9	183770	4	US-09-949-016-15494	Sequence 1494, A	C 329	17	0.9	552	4	US-09-621-576-2814	Sequence 2814, Ap
C 257	18	0.9	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 330	17	0.9	588	4	US-09-902-540-8564	Sequence 8564, Ap
C 258	18	0.9	193303	4	US-09-497-855A-37	Sequence 37, Appl	C 331	17	0.9	601	4	US-09-949-016-19017	Sequence 19017, A
259	18	0.9	199471	4	US-09-949-016-14083	Sequence 14083, A	C 332	17	0.9	601	4	US-09-949-016-19018	Sequence 19018, A
C 260	18	0.9	199471	4	US-09-949-016-14083	Sequence 14083, A	C 333	17	0.9	601	4	US-09-949-016-19019	Sequence 19019, A
C 261	18	0.9	199945	4	US-09-949-016-15436	Sequence 1436, A	C 334	17	0.9	601	4	US-09-949-016-19020	Sequence 19020, A
C 262	18	0.9	202001	4	US-09-734-674-3	Sequence 3, Appl1	C 335	17	0.9	601	4	US-09-949-016-19021	Sequence 19021, A
C 263	18	0.9	206433	4	US-09-949-016-13527	Sequence 1527, A	C 336	17	0.9	601	4	US-09-949-016-20287	Sequence 20287, A
264	18	0.9	212139	4	US-09-949-016-16055	Sequence 16055, A	C 337	17	0.9	601	4	US-09-949-016-20288	Sequence 20288, A
C 265	18	0.9	212139	4	US-09-949-016-16055	Sequence 16055, A	C 338	17	0.9	601	4	US-09-949-016-37001	Sequence 37001, A
C 266	18	0.9	225127	4	US-09-949-016-16480	Sequence 16480, A	C 339	17	0.9	601	4	US-09-949-016-41926	Sequence 41926, A
267	18	0.9	227750	4	US-09-949-016-17175	Sequence 17175, A	C 340	17	0.9	601	4	US-09-949-016-47097	Sequence 47097, A
268	18	0.9	228896	4	US-09-949-016-17127	Sequence 17127, A	C 341	17	0.9	601	4	US-09-949-016-47098	Sequence 47098, A
C 269	18	0.9	232547	4	US-09-949-016-16603	Sequence 16603, A	C 342	17	0.9	601	4	US-09-949-016-47099	Sequence 47099, A
C 270	18	0.9	234864	4	US-09-949-016-16420	Sequence 16420, A	C 343	17	0.9	601	4	US-09-949-016-47100	Sequence 47100, A
C 271	18	0.9	237241	4	US-09-949-016-16101	Sequence 16101, A	C 344	17	0.9	601	4	US-09-949-016-47101	Sequence 47101, A
C 272	18	0.9	237863	4	US-09-949-016-13404	Sequence 13404, A	C 345	17	0.9	601	4	US-09-949-016-49792	Sequence 49792, A
C 273	18	0.9	250715	4	US-09-949-016-13294	Sequence 1294, A	C 346	17	0.9	601	4	US-09-949-016-49793	Sequence 49793, A
274	18	0.9	251769	4	US-09-949-016-13185	Sequence 1185, A	C 347	17	0.9	601	4	US-09-949-016-51297	Sequence 51297, A
C 275	18	0.9	251769	4	US-09-949-016-13185	Sequence 1185, A	C 348	17	0.9	601	4	US-09-949-016-51510	Sequence 51510, A
276	18	0.9	251769	4	US-09-949-016-13186	Sequence 1186, A	C 349	17	0.9	601	4	US-09-949-016-51511	Sequence 51511, A
C 277	18	0.9	251769	4	US-09-949-016-13186	Sequence 1186, A	C 350	17	0.9	601	4	US-09-949-016-51512	Sequence 51512, A
278	18	0.9	254366	4	US-09-822-871-3	Sequence 3, Appl1	C 351	17	0.9	601	4	US-09-949-016-55577	Sequence 55577, A
C 279	18	0.9	254778	4	US-09-949-016-12417	Sequence 12417, A	C 352	17	0.9	601	4	US-09-949-016-55578	Sequence 55578, A
C 280	18	0.9	260286	4	US-09-949-016-17037	Sequence 17037, A	C 353	17	0.9	601	4	US-09-949-016-78056	Sequence 78056, A
C 281	18	0.9	260293	4	US-09-949-016-12106	Sequence 12106, A	C 354	17	0.9	601	4	US-09-949-016-83321	Sequence 83321, A
C 282	18	0.9	266748	4	US-09-949-016-13187	Sequence 13187, A	C 355	17	0.9	601	4	US-09-949-016-83322	Sequence 83322, A
C 283	18	0.9	266748	4	US-09-949-016-13187	Sequence 13187, A	C 356	17	0.9	601	4	US-09-949-016-83326	Sequence 83326, A
284	18	0.9	266748	4	US-09-949-016-13188	Sequence 1188, A	C 357	17	0.9	601	4	US-09-949-016-88218	Sequence 88218, A
C 285	18	0.9	266748	4	US-09-949-016-13188	Sequence 1188, A	C 358	17	0.9	601	4	US-09-949-016-88220	Sequence 88220, A
286	18	0.9	268449	4	US-09-949-016-17244	Sequence 17244, A	C 359	17	0.9	601	4	US-09-949-016-102642	Sequence 102642, A
C 287	18	0.9	294836	4	US-09-949-016-15974	Sequence 15974, A	C 360	17	0.9	601	4	US-09-949-016-102754	Sequence 102754, A
C 288	18	0.9	312470	4	US-09-949-016-14043	Sequence 14043, A	C 361	17	0.9	601	4	US-09-949-016-117074	Sequence 117074, A
289	18	0.9	314798	4	US-09-949-016-13559	Sequence 13559, A	C 362	17	0.9	601	4	US-09-949-016-122238	Sequence 122238, A
290	18	0.9	333820	4	US-09-949-016-14139	Sequence 14139, A	C 363	17	0.9	601	4	US-09-949-016-135078	Sequence 135078, A
291	18	0.9	331814	4	US-09-949-016-12008	Sequence 12008, A	C 364	17	0.9	601	4	US-09-949-016-138709	Sequence 138709, A
292	18	0.9	331814	4	US-09-949-016-17056	Sequence 17056, A	C 365	17	0.9	601	4	US-09-949-016-155193	Sequence 155193, A
C 293	18	0.9	336024	4	US-09-949-016-12373	Sequence 12373, A	C 366	17	0.9	601	4	US-09-949-016-159454	Sequence 159454, A
294	18	0.9	336032	4	US-09-949-016-12415	Sequence 12415, A	C 367	17	0.9	601	4	US-09-949-016-169455	Sequence 169455, A
295	18	0.9	353033	4	US-09-949-016-15754	Sequence 15754, A	C 368	17	0.9	601	4	US-09-949-016-175143	Sequence 175143, A
C 296	18	0.9	385136	4	US-09-949-016-16073	Sequence 16073, A	C 369	17	0.9	601	4	US-09-949-016-175260	Sequence 175260, A
C 297	18	0.9	387902	4	US-09-949-016-14543	Sequence 14543, A	C 370	17	0.9	601	4	US-09-949-016-175262	Sequence 175262, A
C 298	18	0.9	390880	4	US-09-949-016-14720	Sequence 14720, A	C 371	17	0.9	601	4	US-09-949-016-177143	Sequence 177143, A
C 299	18	0.9	421883	4	US-09-949-016-12557	Sequence 12557, A	C 372	17	0.9	601	4	US-09-949-016-181656	Sequence 181656, A
C 300	18	0.9	421883	4	US-09-949-016-15473	Sequence 15473, A	C 373	17	0.9	601	4	US-09-949-016-181656	Sequence 181656, A
C 301	18	0.9	451924	4	US-09-949-016-12896	Sequence 12896, A	C 374	17	0.9	601	4	US-09-949-016-181658	Sequence 181658, A
C 302	18	0.9	451925	4	US-09-949-016-17305	Sequence 17305, A	C 375	17	0.9	601	4	US-09-949-016-181658	Sequence 181658, A
C 303	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 376	17	0.9	601	4	US-09-949-016-189520	Sequence 189520, A
304	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 377	17	0.9	601	4	US-09-949-016-189521	Sequence 189521, A
C 305	18	0.9	462589	4	US-09-949-016-12900	Sequence 12900, A	C 378	17	0.9	601	4	US-09-949-016-189542	Sequence 189542, A
C 306	18	0.9	656591	4	US-09-949-016-11808	Sequence 11808, A	C 379	17	0.9	601	4	US-09-949-016-189543	Sequence 189543, A
C 307	18	0.9	656591	4	US-09-949-016-13368	Sequence 13368, A	C 380	17	0.9	601	4	US-09-949-016-189561	Sequence 189561, A
C 308	18	0.9	678533	4	US-09-949-016-14577	Sequence 14577, A	C 381	17	0.9	601	4	US-09-949-016-189562	Sequence 189562, A
C 309	18	0.9	678533	4	US-09-949-016-14578	Sequence 14578, A	C 382	17	0.9	601	4	US-09-949-016-200004	Sequence 200004, A
310	18	0.9	767677	4	US-09-949-016-12147	Sequence 12147, A	C 383	17	0.9	601	4	US-09-949-016-200005	Sequence 200005, A
311	18	0.9	767677	4	US-09-949-016-17361	Sequence 17361, A	C 384	17	0.9	666	4	US-09-902-540-6479	Sequence 6479, Ap
C 312	17	0.9	786431	4	US-09-751-389-3	Sequence 3, Appl1	C 385	17	0.9	759	4	US-09-620-3120-433	Sequence 433, App
C 313	17	0.9	87	1	US-08-476-860-4	Sequence 4, Appl1	C 386	17	0.9	840	3	US-08-998-4116-507	Sequence 507, App
C 314	17	0.9	87	2	US-08-910-733-4	Sequence 4, Appl1	C 387	17	0.9	967	4	US-09-799-451-396	Sequence 396, App
C 315	17	0.9	212	4	US-09-513-999C-24036	Sequence 24036, A	C 388	17	0.9	1020	4	US-09-454-039A-4899	Sequence 4899, App
C 316	17	0.9	234	4	US-09-313-994C-6650	Sequence 6650, Ap	C 389	17	0.9	1074	4	US-09-512-363-5	Sequence 15, Appl
C 317	17	0.9	324	4	US-09-902-540-2768	Sequence 2768, Ap	C 390	17	0.9	1074	4	US-09-176-200-5	Sequence 5, Appl1
318	17	0.9	353	4	US-09-513-999C-15750	Sequence 15750, A	C 391	17	0.9	1074	4	US-09-915-593-5	Sequence 5, Appl1
319	17	0.9	399	4	US-09-543-681A-1067	Sequence 1067, Ap	C 392	17	0.9	1086	4	US-09-248-796A-6002	Sequence 6002, Ap

C 393	17	0.9	1230	3	US-09-572-191-5	Sequence 5, Appl1	C 466	17	0.9	12565	3	US-09-345-217-3	Sequence 3, Appl1
C 394	17	0.9	1230	3	US-09-723-252-5	Sequence 5, Appl1	C 467	17	0.9	12565	4	US-09-845-129-3	Sequence 3, Appl1
C 395	17	0.9	1230	3	US-09-723-252-5	Sequence 5, Appl1	C 468	17	0.9	12565	4	US-09-578-534-17	Sequence 17, Appl1
C 396	17	0.9	1506	4	US-09-252-991A-811	Sequence 811, Appl	C 469	17	0.9	12565	4	US-09-632-657-3	Sequence 3, Appl1
C 397	17	0.9	1665	4	US-08-812-008-31	Sequence 31, Appl	C 470	17	0.9	12565	4	US-09-584-950-3	Sequence 3, Appl1
C 398	17	0.9	1683	4	US-09-866-510-23	Sequence 23, Appl	C 471	17	0.9	12616	4	US-09-949-016-1347	Sequence 14, Appl1
C 399	17	0.9	1710	4	US-09-248-796A-5020	Sequence 5020, Ap	C 472	17	0.9	14364	4	US-09-949-016-1361	Sequence 13, Appl1
C 400	17	0.9	1789	4	US-09-673-395A-4	Sequence 4, Appl1	C 473	17	0.9	14364	4	US-10-067-443-20	Sequence 20, Appl1
C 401	17	0.9	1839	1	US-08-383-744-1	Sequence 1, Appl1	C 474	17	0.9	15522	4	US-09-902-540-1131	Sequence 11, Appl
C 402	17	0.9	1839	2	US-08-999-336-1	Sequence 1, Appl1	C 475	17	0.9	15522	3	US-09-422-936-60	Sequence 60, Appl
C 403	17	0.9	1839	5	PCT-US96-01427-1	Sequence 19, Appl1	C 476	17	0.9	15849	4	US-09-054-272-50	Sequence 50, Appl
C 404	17	0.9	1890	3	US-08-935-855-19	Sequence 394, Appl	C 477	17	0.9	16311	4	US-09-949-016-12490	Sequence 12, Appl
C 405	17	0.9	1932	4	US-09-949-016-394	Sequence 1526, Ap	C 478	17	0.9	16738	4	US-09-949-016-12168	Sequence 12168, A
C 406	17	0.9	1947	4	US-09-949-016-1526	Sequence 6606, Ap	C 479	17	0.9	16788	4	US-09-949-016-1678	Sequence 14678, A
C 407	17	0.9	1947	4	US-09-902-540-6606	Sequence 501, App	C 480	17	0.9	16802	4	US-09-949-016-1622	Sequence 1622, A
C 408	17	0.9	1951	4	US-09-902-540-501	Sequence 4572, Ap	C 481	17	0.9	16814	4	US-09-949-016-12718	Sequence 12718, A
C 409	17	0.9	2007	4	US-09-252-991A-869	Sequence 869, App	C 482	17	0.9	16874	4	US-09-902-540-15176	Sequence 15176, A
C 410	17	0.9	2097	4	US-09-352-540-4742	Sequence 2268, Ap	C 483	17	0.9	17688	4	US-09-949-016-16718	Sequence 16718, A
C 411	17	0.9	2142	4	US-09-949-016-2268	Sequence 204, App	C 484	17	0.9	18391	4	US-09-949-016-15384	Sequence 15384, A
C 412	17	0.9	2387	4	US-09-614-221A-204	Sequence 459, App	C 485	17	0.9	18798	3	US-09-272-032-8	Sequence 8, Appl1
C 413	17	0.9	2409	4	US-09-902-540-459	Sequence 13, Appl	C 486	17	0.9	19056	4	US-09-443-218-8	Sequence 8, Appl1
C 414	17	0.9	3134	4	US-09-866-510-13	Sequence 15, Appl	C 487	17	0.9	19056	4	US-09-949-016-17126	Sequence 17126, A
C 415	17	0.9	3321	4	US-09-866-510-15	Sequence 17, Appl	C 488	17	0.9	22975	4	US-09-902-540-1233	Sequence 1233, Ap
C 416	17	0.9	3321	4	US-09-866-510-17	Sequence 19, Appl	C 489	17	0.9	22975	4	US-09-949-016-16707	Sequence 16707, A
C 417	17	0.9	3331	4	US-09-866-510-19	Sequence 21, Appl	C 490	17	0.9	22524	4	US-09-949-016-1233	Sequence 1233, Ap
C 418	17	0.9	3331	4	US-09-866-510-21	Sequence 1919, Ap	C 491	17	0.9	22524	4	US-09-949-016-16707	Sequence 16707, A
C 419	17	0.9	3422	4	US-09-949-016-1919	Sequence 62, App	C 492	17	0.9	22521	4	US-09-949-016-14390	Sequence 14390, A
C 420	17	0.9	3430	4	US-09-949-016-1880	Sequence 889, App	C 493	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 421	17	0.9	3430	4	US-09-949-016-1880	Sequence 748, App	C 494	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 422	17	0.9	3430	4	US-09-949-016-1880	Sequence 8, Appl1	C 495	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 423	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 496	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 424	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 497	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 425	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 498	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 426	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 499	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 427	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 500	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 428	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 501	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 429	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 502	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 430	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 503	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 431	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 504	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
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C 433	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 506	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 434	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 507	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
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C 441	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 514	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
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C 443	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 516	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
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C 451	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 524	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 452	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 525	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 453	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 526	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 454	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 527	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 455	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 528	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 456	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 529	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
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C 460	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 533	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 461	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 534	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 462	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 535	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 463	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 536	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 464	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 537	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A
C 465	17	0.9	4076	4	US-09-573-080A-62	Sequence 8, Appl1	C 538	17	0.9	22582	4	US-09-949-016-14390	Sequence 14390, A

539	17	0.9	97221	4	US-09-949-016-12755	Sequence 12755, A	612	16	0.8	95	1	US-08-180-195-17	Sequence 17, Appl
C 540	17	0.9	103712	4	US-09-949-016-13058	Sequence 13058, A	C 613	16	0.8	95	1	US-08-477-329-16	Sequence 17, Appl
C 541	17	0.9	107800	4	US-09-949-016-13118	Sequence 13118, A	C 614	16	0.8	95	1	US-08-477-329-16	Sequence 17, Appl
C 542	17	0.9	111677	4	US-09-949-016-16966	Sequence 16966, A	C 615	16	0.8	95	2	US-08-475-458-16	Sequence 16, Appl
C 543	17	0.9	116425	4	US-09-949-016-11809	Sequence 11809, A	C 616	16	0.8	95	2	US-08-475-458-17	Sequence 17, Appl
C 544	17	0.9	119032	4	US-09-949-016-12160	Sequence 12160, A	C 617	16	0.8	95	3	US-08-960-400-16	Sequence 17, Appl
C 545	17	0.9	119032	4	US-09-949-016-17268	Sequence 17268, A	C 618	16	0.8	95	3	US-08-960-400-17	Sequence 17, Appl
C 546	17	0.9	121427	4	US-09-949-016-11950	Sequence 11950, A	C 619	16	0.8	95	3	US-08-980-400-17	Sequence 17, Appl
C 547	17	0.9	121433	4	US-09-949-016-13230	Sequence 13230, A	C 620	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
C 548	17	0.9	125672	4	US-09-949-016-16956	Sequence 16956, A	C 621	16	0.8	95	3	US-09-583-459A-17	Sequence 17, Appl
549	17	0.9	128779	4	US-09-487-855A-38	Sequence 38, Appl	C 622	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
550	17	0.9	130724	4	US-09-949-016-13753	Sequence 13753, A	C 623	16	0.8	95	3	US-09-583-459A-16	Sequence 16, Appl
551	17	0.9	130971	4	US-09-949-016-14205	Sequence 14205, A	C 624	16	0.8	95	3	US-09-583-459A-17	Sequence 17, Appl
552	17	0.9	143550	4	US-09-949-016-14113	Sequence 14113, A	C 625	16	0.8	95	3	US-09-435-059-16	Sequence 16, Appl
553	17	0.9	146307	4	US-09-949-016-14881	Sequence 14881, A	C 626	16	0.8	95	3	US-09-435-059-17	Sequence 17, Appl
554	17	0.9	146307	4	US-09-949-016-14882	Sequence 14882, A	C 627	16	0.8	107	4	US-09-513-999C-18689	Sequence 18689, A
555	17	0.9	146307	4	US-09-949-016-14883	Sequence 14883, A	C 628	16	0.8	124	4	US-09-513-999C-15500	Sequence 15500, A
556	17	0.9	146307	4	US-09-949-016-14884	Sequence 14884, A	C 629	16	0.8	124	4	US-09-513-999C-18688	Sequence 18688, A
557	17	0.9	146307	4	US-09-949-016-14885	Sequence 14885, A	C 630	16	0.8	124	4	US-09-513-999C-18688	Sequence 18688, A
558	17	0.9	146307	4	US-09-949-016-14886	Sequence 14886, A	C 631	16	0.8	124	4	US-09-513-999C-18688	Sequence 18688, A
559	17	0.9	146307	4	US-09-949-016-14887	Sequence 14887, A	C 632	16	0.8	124	4	US-09-513-999C-18688	Sequence 18688, A
560	17	0.9	146307	4	US-09-949-016-14888	Sequence 14888, A	C 633	16	0.8	124	4	US-09-513-999C-18688	Sequence 18688, A
561	17	0.9	148405	4	US-09-949-016-11747	Sequence 11747, A	C 634	16	0.8	201	4	US-09-248-796A-8710	Sequence 8710, Ap
562	17	0.9	148405	4	US-09-949-016-12835	Sequence 12835, A	C 635	16	0.8	220	4	US-09-621-976-15613	Sequence 15613, A
563	17	0.9	148405	4	US-09-949-016-12836	Sequence 12836, A	C 636	16	0.8	220	4	US-09-513-999C-3202	Sequence 3202, A
564	17	0.9	148405	4	US-09-949-016-12837	Sequence 12837, A	C 637	16	0.8	223	4	US-09-513-999C-24058	Sequence 24058, A
565	17	0.9	149543	4	US-09-949-016-15947	Sequence 15947, A	C 638	16	0.8	269	4	US-09-513-999C-2438	Sequence 2438, Ap
566	17	0.9	150409	4	US-09-949-016-12928	Sequence 12920, A	C 639	16	0.8	269	4	US-09-513-999C-2438	Sequence 2438, Ap
567	17	0.9	152524	4	US-09-949-016-12928	Sequence 12928, A	C 640	16	0.8	269	4	US-09-513-999C-14847	Sequence 14847, A
568	17	0.9	152524	4	US-09-949-016-12663	Sequence 12663, A	C 641	16	0.8	301	4	US-09-513-999C-14847	Sequence 14847, A
569	17	0.9	152524	4	US-09-949-016-13194	Sequence 13194, A	C 642	16	0.8	319	3	US-08-905-223-47	Sequence 47, Appl
570	17	0.9	161124	4	US-09-949-016-11760	Sequence 11760, A	C 643	16	0.8	338	4	US-09-513-999C-32601	Sequence 32601, A
C 571	17	0.9	174030	4	US-09-949-016-12610	Sequence 12610, A	C 644	16	0.8	339	4	US-09-621-976-15613	Sequence 15613, A
C 572	17	0.9	174030	4	US-09-949-016-13880	Sequence 13880, A	C 645	16	0.8	334	4	US-09-270-767-7566	Sequence 7566, Ap
C 573	17	0.9	177293	4	US-09-949-016-16513	Sequence 16513, A	C 646	16	0.8	334	4	US-09-270-767-7566	Sequence 7566, Ap
C 574	17	0.9	193169	4	US-09-949-016-15091	Sequence 15091, A	C 647	16	0.8	337	4	US-09-513-999C-3683	Sequence 3683, Ap
C 575	17	0.9	194889	4	US-09-949-016-15654	Sequence 15654, A	C 648	16	0.8	348	2	US-08-944-449-1	Sequence 17, Appl
576	17	0.9	218940	4	US-09-949-016-17539	Sequence 17539, A	C 649	16	0.8	348	5	PCT-US95-08492-17	Sequence 17, Appl
C 577	17	0.9	227390	4	US-09-949-016-12201	Sequence 12201, A	C 650	16	0.8	348	5	PCT-US95-08492-17	Sequence 17, Appl
C 578	17	0.9	227391	4	US-09-949-016-13365	Sequence 13365, A	C 651	16	0.8	351	4	US-09-513-999C-3315	Sequence 3315, A
C 579	17	0.9	250352	4	US-09-949-016-14724	Sequence 14724, A	C 652	16	0.8	351	4	US-09-513-999C-3315	Sequence 3315, A
580	17	0.9	256171	4	US-09-949-016-12822	Sequence 12822, A	C 653	16	0.8	358	4	US-09-513-999C-33751	Sequence 33751, A
581	17	0.9	256176	4	US-09-949-016-15524	Sequence 15524, A	C 654	16	0.8	378	4	US-09-513-999C-33751	Sequence 33751, A
582	17	0.9	278866	4	US-09-949-016-13922	Sequence 13922, A	C 655	16	0.8	381	3	US-09-621-976-11433	Sequence 11433, A
583	17	0.9	278866	4	US-09-949-016-13923	Sequence 13923, A	C 656	16	0.8	381	3	US-09-621-976-11433	Sequence 11433, A
584	17	0.9	278866	4	US-09-949-016-13924	Sequence 13924, A	C 657	16	0.8	383	4	US-09-312-283C-3	Sequence 3, Appl
585	17	0.9	278866	4	US-09-949-016-13925	Sequence 13925, A	C 658	16	0.8	383	4	US-09-312-283C-3	Sequence 3, Appl
586	17	0.9	278866	4	US-09-949-016-13926	Sequence 13926, A	C 659	16	0.8	393	2	US-08-944-449-1	Sequence 7, Appl
587	17	0.9	278866	4	US-09-949-016-14699	Sequence 14699, A	C 660	16	0.8	393	3	US-09-513-999C-1343	Sequence 1343, A
588	17	0.9	278866	4	US-09-949-016-14700	Sequence 14700, A	C 661	16	0.8	402	4	US-09-513-999C-287	Sequence 287, Ap
589	17	0.9	278866	4	US-09-949-016-14701	Sequence 14701, A	C 662	16	0.8	420	4	US-09-489-039A-4159	Sequence 4159, Ap
590	17	0.9	278866	4	US-09-949-016-14702	Sequence 14702, A	C 663	16	0.8	420	4	US-09-489-039A-4159	Sequence 4159, Ap
591	17	0.9	278866	4	US-09-949-016-14703	Sequence 14703, A	C 664	16	0.8	420	4	US-09-489-039A-4159	Sequence 4159, Ap
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C 593	17	0.9	392000	4	US-10-027-983-11	Sequence 11, Appl	C 666	16	0.8	440	4	US-09-270-767-8160	Sequence 8160, Ap
C 594	17	0.9	421118	4	US-09-949-016-16297	Sequence 16297, A	C 667	16	0.8	452	4	US-09-497-855A-31	Sequence 31, Appl
C 595	17	0.9	4403765	3	US-09-790-988-1	Sequence 1, Appl	C 668	16	0.8	459	4	US-09-854-133-565	Sequence 565, Ap
596	17	0.9	4411529	3	US-09-103-840A-2	Sequence 2, Appl	C 669	16	0.8	462	4	US-09-854-133-565	Sequence 565, Ap
597	17	0.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl	C 670	16	0.8	462	4	US-09-854-133-565	Sequence 565, Ap
598	16	0.8	20	1	US-08-480-784-9	Sequence 9, Appl	C 671	16	0.8	462	4	US-09-854-133-565	Sequence 565, Ap
599	16	0.8	20	1	US-08-483-553-9	Sequence 9, Appl	C 672	16	0.8	462	4	US-09-854-133-565	Sequence 565, Ap
600	16	0.8	20	1	US-08-487-002-9	Sequence 9, Appl	C 673	16	0.8	471	4	US-09-270-767-16306	Sequence 16306, A
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602	16	0.8	20	1	US-08-483-554B-9	Sequence 9, Appl	C 675	16	0.8	471	4	US-09-270-767-16306	Sequence 16306, A
603	16	0.8	20	1	US-08-488-011B-9	Sequence 9, Appl	C 676	16	0.8	477	4	US-09-513-999C-11548	Sequence 11548, A
604	16	0.8	20	5	US-08-850-727-9	Sequence 9, Appl	C 677	16	0.8	487	4	US-09-513-999C-11548	Sequence 11548, A
605	16	0.8	20	5	PCT-US95-10202-9	Sequence 9, Appl	C 678	16	0.8	510	4	US-09-621-976-18210	Sequence 18210, A
606	16	0.8	20	5	PCT-US95-10203-9	Sequence 9, Appl	C 679	16	0.8	511	3	US-09-621-976-18210	Sequence 18210, A
607	16	0.8	25	4	US-09-396-196G-30034	Sequence 30034, A	C 680	16	0.8	513	4	US-09-621-976-18210	Sequence 18210, A
C 608	16	0.8	28	1	US-08-723-896G-15	Sequence 15, Appl	C 681	16	0.8	513	4	US-09-621-976-18210	Sequence 18210, A
C 609	16	0.8	28	3	US-08-424-797A-15	Sequence 15, Appl	C 682	16	0.8	532	4	US-09-621-976-18210	Sequence 18210, A
C 610	16	0.8	84	1	US-08-424-583-7	Sequence 7, Appl	C 683	16	0.8	534	4	US-09-621-976-18210	Sequence 18210, A
C 611	16	0.8	95	1	US-08-180-195-16	Sequence 16, Appl	C 684	16	0.8	540	4	US-09-621-976-18210	Sequence 18210, A

C 685	16	0.8	576	4	US-09-976-594-839	Sequence 839, App
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C 687	16	0.8	601	4	US-09-949-016-19012	Sequence 19012, A
C 688	16	0.8	601	4	US-09-949-016-19013	Sequence 19013, A
C 689	16	0.8	601	4	US-09-949-016-20316	Sequence 20316, A
C 690	16	0.8	601	4	US-09-949-016-20399	Sequence 20399, A
C 691	16	0.8	601	4	US-09-949-016-21548	Sequence 21548, A
C 692	16	0.8	601	4	US-09-949-016-21549	Sequence 21549, A
C 693	16	0.8	601	4	US-09-949-016-26532	Sequence 26532, A
C 694	16	0.8	601	4	US-09-949-016-27931	Sequence 27931, A
C 695	16	0.8	601	4	US-09-949-016-29021	Sequence 29021, A
C 696	16	0.8	601	4	US-09-949-016-29022	Sequence 29022, A
C 697	16	0.8	601	4	US-09-949-016-29023	Sequence 29023, A
C 698	16	0.8	601	4	US-09-949-016-29024	Sequence 29024, A
C 699	16	0.8	601	4	US-09-949-016-29025	Sequence 29025, A
C 700	16	0.8	601	4	US-09-949-016-29026	Sequence 29026, A
C 701	16	0.8	601	4	US-09-949-016-29419	Sequence 29419, A
C 702	16	0.8	601	4	US-09-949-016-31842	Sequence 31842, A
C 703	16	0.8	601	4	US-09-949-016-31843	Sequence 31843, A
C 704	16	0.8	601	4	US-09-949-016-35934	Sequence 35934, A
C 705	16	0.8	601	4	US-09-949-016-37893	Sequence 37893, A
C 706	16	0.8	601	4	US-09-949-016-38379	Sequence 38379, A
C 707	16	0.8	601	4	US-09-949-016-39318	Sequence 39318, A
C 708	16	0.8	601	4	US-09-949-016-39350	Sequence 39350, A
C 709	16	0.8	601	4	US-09-949-016-39382	Sequence 39382, A
C 710	16	0.8	601	4	US-09-949-016-39414	Sequence 39414, A
C 711	16	0.8	601	4	US-09-949-016-46984	Sequence 46984, A
C 712	16	0.8	601	4	US-09-949-016-47092	Sequence 47092, A
C 713	16	0.8	601	4	US-09-949-016-47093	Sequence 47093, A
C 714	16	0.8	601	4	US-09-949-016-47541	Sequence 47541, A
C 715	16	0.8	601	4	US-09-949-016-48081	Sequence 48081, A
C 716	16	0.8	601	4	US-09-949-016-48476	Sequence 48476, A
C 717	16	0.8	601	4	US-09-949-016-52557	Sequence 52557, A
C 718	16	0.8	601	4	US-09-949-016-52558	Sequence 52558, A
C 719	16	0.8	601	4	US-09-949-016-53369	Sequence 53369, A
C 720	16	0.8	601	4	US-09-949-016-53420	Sequence 53420, A
C 721	16	0.8	601	4	US-09-949-016-53421	Sequence 53421, A
C 722	16	0.8	601	4	US-09-949-016-55066	Sequence 55066, A
C 723	16	0.8	601	4	US-09-949-016-55067	Sequence 55067, A
C 724	16	0.8	601	4	US-09-949-016-55068	Sequence 55068, A
C 725	16	0.8	601	4	US-09-949-016-55069	Sequence 55069, A
C 726	16	0.8	601	4	US-09-949-016-55070	Sequence 55070, A
C 727	16	0.8	601	4	US-09-949-016-55071	Sequence 55071, A
C 728	16	0.8	601	4	US-09-949-016-55072	Sequence 55072, A
C 729	16	0.8	601	4	US-09-949-016-55073	Sequence 55073, A
C 730	16	0.8	601	4	US-09-949-016-55074	Sequence 55074, A
C 731	16	0.8	601	4	US-09-949-016-55075	Sequence 55075, A
C 732	16	0.8	601	4	US-09-949-016-55076	Sequence 55076, A
C 733	16	0.8	601	4	US-09-949-016-55077	Sequence 55077, A
C 734	16	0.8	601	4	US-09-949-016-55078	Sequence 55078, A
C 735	16	0.8	601	4	US-09-949-016-55079	Sequence 55079, A
C 736	16	0.8	601	4	US-09-949-016-55080	Sequence 55

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832	16	0.8	601	4	US-09-949-016-110696	Sequence 110696,	905	16	0.8	601	4	US-09-949-016-167373	Sequence 167373,
833	16	0.8	601	4	US-09-949-016-110697	Sequence 110697,	c 906	16	0.8	601	4	US-09-949-016-167510	Sequence 167510,
834	16	0.8	601	4	US-09-949-016-113879	Sequence 113879,	907	16	0.8	601	4	US-09-949-016-170138	Sequence 170138,
835	16	0.8	601	4	US-09-949-016-114047	Sequence 114047,	908	16	0.8	601	4	US-09-949-016-170168	Sequence 170168,
836	16	0.8	601	4	US-09-949-016-114215	Sequence 114215,	909	16	0.8	601	4	US-09-949-016-172097	Sequence 172097,
837	16	0.8	601	4	US-09-949-016-114383	Sequence 114383,	c 910	16	0.8	601	4	US-09-949-016-172623	Sequence 172623,
838	16	0.8	601	4	US-09-949-016-114551	Sequence 114551,	911	16	0.8	601	4	US-09-949-016-175556	Sequence 175556,
839	16	0.8	601	4	US-09-949-016-114719	Sequence 114719,	c 912	16	0.8	601	4	US-09-949-016-175556	Sequence 175556,
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841	16	0.8	601	4	US-09-949-016-115055	Sequence 115055,	914	16	0.8	601	4	US-09-949-016-176214	Sequence 176214,
c 842	16	0.8	601	4	US-09-949-016-117077	Sequence 117077,	915	16	0.8	601	4	US-09-949-016-176993	Sequence 176993,
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847	16	0.8	601	4	US-09-949-016-121539	Sequence 121539,	c 920	16	0.8	601	4	US-09-949-016-178231	Sequence 178231,
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852	16	0.8	601	4	US-09-949-016-123235	Sequence 123235,	925	16	0.8	601	4	US-09-949-016-179326	Sequence 179326,
853	16	0.8	601	4	US-09-949-016-123239	Sequence 123239,	c 926	16	0.8	601	4	US-09-949-016-179787	Sequence 179787,
854	16	0.8	601	4	US-09-949-016-123313	Sequence 123313,	c 927	16	0.8	601	4	US-09-949-016-180672	Sequence 180672,
855	16	0.8	601	4	US-09-949-016-123413	Sequence 123413,	c 928	16	0.8	601	4	US-09-949-016-181652	Sequence 181652,
856	16	0.8	601	4	US-09-949-016-123455	Sequence 123455,	c 929	16	0.8	601	4	US-09-949-016-181653	Sequence 181653,
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858	16	0.8	601	4	US-09-949-016-123539	Sequence 123539,	c 931	16	0.8	601	4	US-09-949-016-184667	Sequence 184667,
859	16	0.8	601	4	US-09-949-016-123581	Sequence 123581,	c 932	16	0.8	601	4	US-09-949-016-184668	Sequence 184668,
860	16	0.8	601	4	US-09-949-016-123623	Sequence 123623,	c 933	16	0.8	601	4	US-09-949-016-184669	Sequence 184669,
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862	16	0.8	601	4	US-09-949-016-123707	Sequence 123707,	935	16	0.8	601	4	US-09-949-016-184808	Sequence 184808,
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872	16	0.8	601	4	US-09-949-016-132854	Sequence 132854,	945	16	0.8	601	4	US-09-949-016-192451	Sequence 192451,
c 873	16	0.8	601	4	US-09-949-016-135244	Sequence 135244,	c 946	16	0.8	601	4	US-09-949-016-193897	Sequence 193897,
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c 875	16	0.8	601	4	US-09-949-016-138084	Sequence 138084,	948	16	0.8	601	4	US-09-949-016-195473	Sequence 195473,
c 876	16	0.8	601	4	US-09-949-016-138720	Sequence 138720,	c 949	16	0.8	601	4	US-09-949-016-195928	Sequence 195928,
c 877	16	0.8	601	4	US-09-949-016-138721	Sequence 138721,	950	16	0.8	601	4	US-09-949-016-196812	Sequence 196812,
c 878	16	0.8	601	4	US-09-949-016-138722	Sequence 138722,	951	16	0.8	601	4	US-09-949-016-196840	Sequence 196840,
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c 880	16	0.8	601	4	US-09-949-016-139654	Sequence 139654,	953	16	0.8	601	4	US-09-949-016-201865	Sequence 201865,
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c 886	16	0.8	601	4	US-09-949-016-149076	Sequence 149076,	959	16	0.8	601	4	US-09-949-016-205504	Sequence 205504,
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c 888	16	0.8	601	4	US-09-949-016-151918	Sequence 151918,	c 961	16	0.8	601	4	US-09-949-016-205545	Sequence 205545,
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c 894	16	0.8	601	4	US-09-949-016-157096	Sequence 157096,	c 967	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
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897	16	0.8	601	4	US-09-949-016-157589	Sequence 157589,	c 970	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 898	16	0.8	601	4	US-09-949-016-159077	Sequence 159077,	971	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 899	16	0.8	601	4	US-09-949-016-160640	Sequence 160640,	c 972	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
900	16	0.8	601	4	US-09-949-016-160641	Sequence 160641,	c 973	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
901	16	0.8	601	4	US-09-949-016-160641	Sequence 160641,	c 974	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 902	16	0.8	601	4	US-09-949-016-163039	Sequence 163039,	975	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,
c 903	16	0.8	601	4	US-09-949-016-163040	Sequence 163040,	976	16	0.8	601	4	US-09-949-016-206535	Sequence 206535,

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RESULT 1
US-09-621-976-3396
; Sequence 3396, Application US/09621976
; Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: GENSET 054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3396
LENGTH: 316
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 66..311
NAME/KEY: miscFeature
LOCATION: 301
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-3396

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RESULT 2
US-09-489-039A-6886
; Sequence 6886, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

Sequence 7101, Ap
Sequence 15, Appl
Sequence 854, App
Sequence 1268, Ap
Sequence 1477, Ap
Sequence 1477, Ap
Sequence 1477, Ap
Sequence 1477, Ap
Sequence 1477, Ap
Sequence 8, Appl
Sequence 8, Appl
Sequence 141, Appl
Sequence 1417, Ap
Sequence 882, App
Sequence 1979, Ap
Sequence 5414, Ap
Sequence 20696, A
Sequence 3191, Ap
Sequence 282, App
Sequence 8694, Ap
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl

: APPLICANT: Gary Breton et. al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
: FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
: CURRENT APPLICATION NUMBER: US/09/489,039A
: PRIOR FILING DATE: 2000-01-27
: PRIOR APPLICATION NUMBER: US 60/117,747
: PRIOR FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 14342
: SEQ ID NO: 6886
: LENGTH: 792
: TYPE: DNA
: ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6886

Query Match 1.1%; Score 20; DB 4; Length 792;
Best Local Similarity 100.0%; Pred.No.22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1288 CTGTCATCGCAACAGGT 1307
 |||||
Db 68 CTGTCATCGCAACCAGT 87

```

? sequence 7008, Application US/09469039A
? Patent No. 6610836
?
? GENERAL INFORMATION:
? APPLICANT: Gary Breton et. al
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
? TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 2709.2004001
? CURRENT APPLICATION NUMBER: US/09/469,039A
? PRIOR FILING DATE: 2000-01-27
? PRIOR APPLICATION NUMBER: US 60/117,747
? PRIOR FILING DATE: 1999-01-29
? NUMBER OF SEQ ID NOS: 14342
? SEQ ID NO 7008
? LENGTH: 1701
? TYPE: DNA
? ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7008

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	Query Match	1.1%;	Score 20;	DB 4;	Length 1701;	
	Best Local Similarity	100.0%;	Pred. No. 21;			
	Matches	20;	Conservative	0;	Mismatches	0;
Qy	1288 CMTGTCATCGGCACCAACCCAGGT	1307				
Dd	a2 CMTGTCATCGGCACCAACCCAGGT	101				

US-CV-1745-206A-14/C
Sequence 14, Application US/07745206A
Patent No. 5429921
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McGuire, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2470 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2469
US-07-745-206A-14

Query Match 1.1%; Score 20; DB 1; Length 2470;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
Db 1856 AACAGGAAGCAAGAG 1837

RESULT 5
US-08-311-363-14/c
Sequence 14, Application US/08311363
Patent No. 5876958
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2470 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2469
US-08-311-363-14

Query Match 1.1%; Score 20; DB 2; Length 2470;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
Db 1856 AACAGGAAGCAAGAG 1837

RESULT 6
US-07-745-206A-12/c
Sequence 12, Application US/07745206A
Patent No. 5429921
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5467 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 61n(144..3164, 3168..3245, 3249..3386, 3390
..3392, 3396..3488, 3495..3539, 3543..3581, 3585
..3587, 3591..3626, 3630..3689, 3693..3737, 3744
..3746, 3750..4823, 4827..4841, 4845..5006, 5010
..5096, 5100..5306, 5310..5366, 5370..5465)
US-07-745-206A-12

Query Match 1.1%; Score 20; DB 1; Length 5467;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 1999 AACAGAGAGCAGAGAG 1980

RESULT 7

US-08-311-363-12/c
; Sequence 12, Application US/08311363
; Patent No. 5876958
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: Human Calcium Channel Compositions and
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,363
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-51506
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(144..3164, 3168..3245, 3249..3386, 3390
; ..3392, 3396..3488, 3495..3539, 3543..3581, 3585
; ..3587, 3591..3626, 3630..3689, 3693..3737, 3744
; ..3746, 3750..4823, 4827..4841, 4845..5006, 5010
; ..5096, 5100..5306, 5310..5366, 5370..5465)
US-08-311-363-12

Query Match 1.1%; Score 20; DB 2; Length 5467;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 1999 AACAGAGAGCAGAGAG 1980

RESULT 8

US-08-456-200B-11/c
; Sequence 11, Application US/08456200B
; Patent No. 6229000
; GENERAL INFORMATION:
; APPLICANT: Franz, Jürgen; Weingartner, Bernhard;
; APPLICANT: Unterbeck, Axel; Rae, Peter
; TITLE OF INVENTION: TISSUE-SPECIFIC HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUB-TYPES AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: NEC Powermate SX/20
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,200B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/094,712
; FILING DATE: 19-JUL-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/858,278
; FILING DATE: 26-MAR-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/064,778
; FILING DATE: 19-MAY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: DE 41 10 785
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 8398.3-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TEXT:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6232 nucleotides
; TYPE: Nucleotide
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: CDNA
US-08-456-200B-11

Query Match 1.1%; Score 20; DB 3; Length 6232;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGAGAGCAGAGAG 720
DB 887 AACAGAGAGCAGAGAG 868

RESULT 9

US-08-455-543A-8/c
; Sequence 8, Application US/0845543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-455-543A-8

Query Match 1.1%; Score 20; DB 1; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 701 AACGGAAGACCAAGAG 720
DB 1999 AACGGAAGACCAAGAG 1980

RESULT 10
US-08-193-078B-8/c
Sequence 8, Application US/08193078B
Patent No. 5846757
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
STREET: 1660 UNION STREET
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,078B
FILING DATE: 07-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-53607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-193-078B-8

Query Match 1.1%; Score 20; DB 2; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1999 AACAGGAGCAGAGAG 1980

RESULT 11

US-08-223-305C-8/c

Sequence 8, Application US/08223305C

Patent No. 5851824

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/223,305C

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 52516 (P519739)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 7175 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 144..6857

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..143

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 6855..7175

US-08-223-305C-8

Query Match 1.1% Score 20; DB 2; Length 7175;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAGCAGAGAG 720

Db 1999 AACAGGAGCAGAGAG 1980

RESULT 12

US-08-149-097D-8/c

Sequence 8, Application US/08149097D

Patent No. 5874236

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,097D

FILING DATE: 05-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/105,536

FILING DATE: 11-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US92/06903

FILING DATE: 14-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,231

FILING DATE: 13-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/868,354

FILING DATE: 10-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FLING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0062
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 6855..7175
US-08-149-097D-8

Query Match 1.1%; Score 20; DB 2; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 701 AACGAGAGCAAGAG 720
Db 1999 AACGAGAGCAAGAG 1980

RESULT 13
US-08-949-386-8/c
Sequence 8, Application US/08949386
Patent No. 6090623
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Allison
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,386
FLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/290,012
FLING DATE: 11-AUG-1994
APPLICATION NUMBER: 08/149,097
FLING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FLING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 519808
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0062
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5' UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3' UTR
LOCATION: 6855..7175
US-08-949-386-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 701 AACGAGAGCAAGAG 720
Db 1999 AACGAGAGCAAGAG 1980

RESULT 14
US-08-450-562-8/c
Sequence 8, Application US/08450562
Patent No. 6096514
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Gillespie, Allison
APPLICANT: Feldman, Daniel
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: US
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,562
FLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,950
FLING DATE: 13-MAR-1995
APPLICATION NUMBER: 08/336,257
FLING DATE: 7-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,083
FLING DATE: 28-SEPT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/311,363
FILING DATE: 23-SEPT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,012
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: 4-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/193,078
FILING DATE: 07-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,097
FILING DATE: 5-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,536
FILING DATE: 11-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,231
FILING DATE: 13-JULY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: 10-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06903
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/603,751
FILING DATE: 08-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/482,384
FILING DATE: 02-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-519812
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-450-562-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
DB 1999 AACAGGAAGCAAGAG 1980

RESULT 15
US-08-984-709A-8/C
Sequence 8, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7175 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..6857
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 6855..7175
US-08-984-709A-8

Query Match 1.1%; Score 20; DB 3; Length 7175;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 AACAGGAAGCAAGAG 720
DB 1999 AACAGGAAGCAAGAG 1980

Search completed: March 8, 2005, 01:45:00
Job time : 373 secs